EXHIBIT 1

US010900034B2

(12) United States Patent

Ryan et al.

(10) Patent No.: US 10,900,034 B2
(45) Date of Patent: *Jan. 26, 2021

(54) **GUIDE RNA WITH CHEMICAL MODIFICATIONS**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 708 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: **14/757,204**

(22) Filed: **Dec. 3, 2015**

(65) **Prior Publication Data**

US 2016/0289675 A1 Oct. 6, 2016

Related U.S. Application Data

(60) Provisional application No. 62/256,095, filed on Nov. 16, 2015, provisional application No. 62/146,189, filed on Apr. 10, 2015, provisional application No. 62/087,211, filed on Dec. 3, 2014.

(51) **Int. Cl.**

C12N 15/113	(2010.01)
C12N 9/22	(2006.01)
C12N 15/11	(2006.01)
C07H 21/02	(2006.01)
C12N 15/90	(2006.01)
C12Q 1/6876	(2018.01)

(52) **U.S. Cl.**

CPC ***C12N 15/111*** (2013.01); ***C07H 21/02*** (2013.01); ***C12N 9/22*** (2013.01); ***C12N 15/113*** (2013.01); ***C12N 15/907*** (2013.01); ***C12Q 1/6876*** (2013.01); *C12N 2310/10* (2013.01); *C12N 2310/20* (2017.05); *C12N 2310/312* (2013.01); *C12N 2310/315* (2013.01); *C12N 2310/321* (2013.01); *C12N 2310/322* (2013.01); *C12N 2310/323* (2013.01); *C12N 2310/3231* (2013.01); *C12N 2310/333* (2013.01); *C12N 2310/335* (2013.01); *C12N 2310/346* (2013.01); *C12N 2310/3517* (2013.01); *C12N 2310/531* (2013.01); *C12N 2320/51* (2013.01); *C12N 2320/53* (2013.01); *C12N 2330/31* (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to modified guide RNAs and their use in clustered, regularly interspaced, short palindromic repeats (CRISPR)/CRISPR-associated (Cas) systems.

33 Claims, 18 Drawing Sheets

Specification includes a Sequence Listing.

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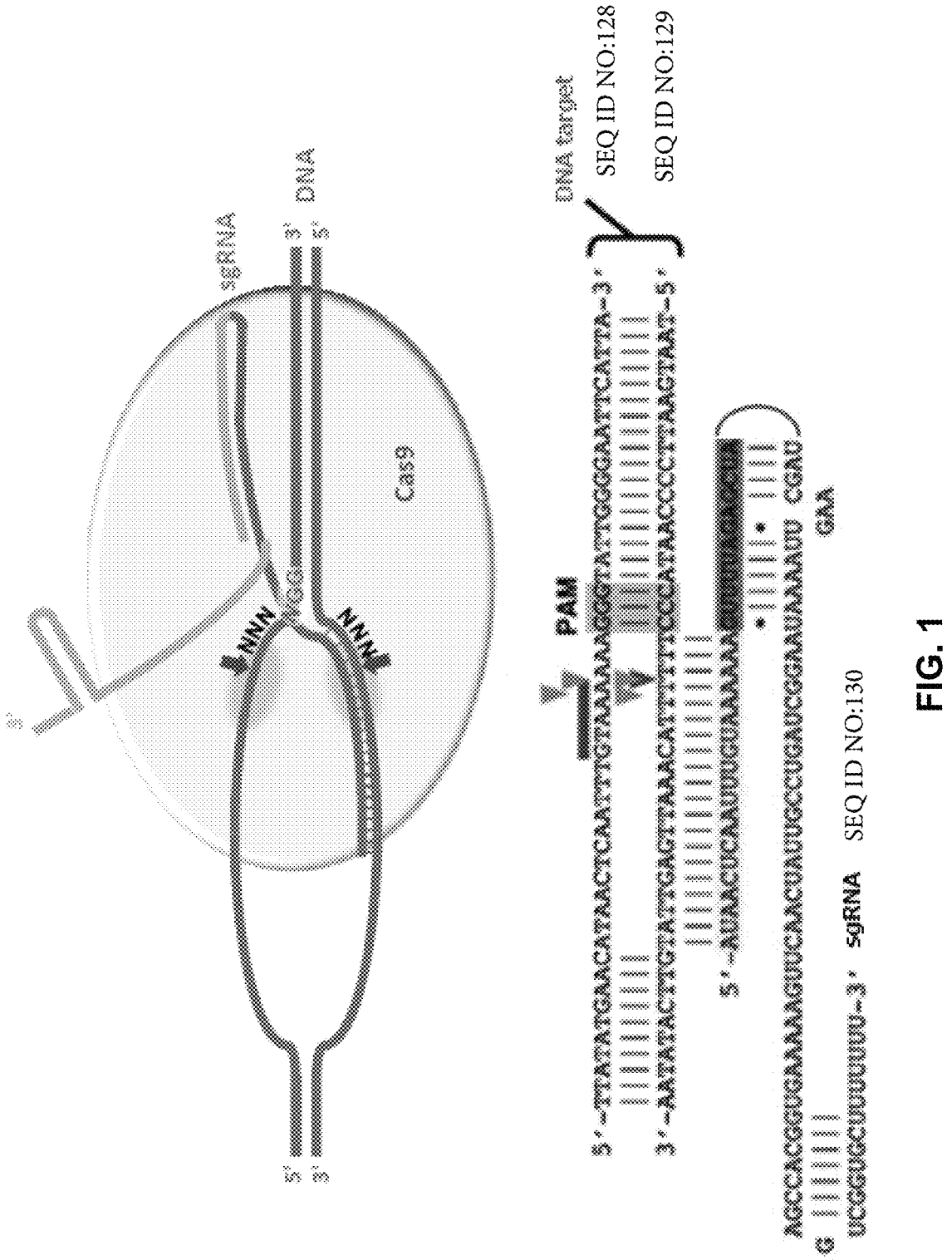
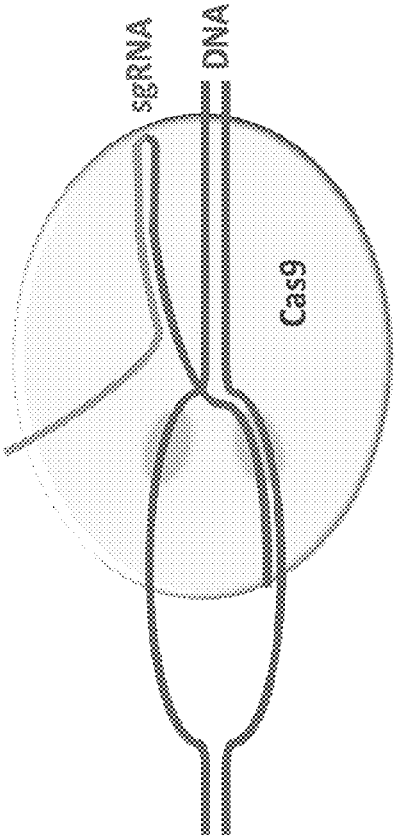

sgRNA
3'
5'
DNA
Cas9
NNN
NNN
5'
3'
DNA target
SEQ ID NO:128
SEQ ID NO:129
PAM
5'-TTATATGAACATTTGTAAAAAGGTATTGGGAATTCATTA-3'
3'-AATATACTTGTAATTGAGTTAAACATTTTTCCATAACCCTTAAGTAAT-5'
5'-AUAACUCAAUUUGUAAAAAG
AGCACGGUGAAAAAGUUCAACUAUUGCCUGAUCGGAAUAAAAUU CGAU
GAA
G
UCGGUGCUUUUUUUU-3' sgRNA SEQ ID NO:130

FIG. 1

FINAL CONC. in	20 uL cleavage rxn
Rxn volume	20 µL
Cas9 protein	40 nM (125 ng/20 uL rxn)
Guide RNA	50 nM
Target DNA	2.6 nM
TrisHCl pH 7.6	100 mM
NaCl	50 mM
$MgCl_2$	10 mM

FIG. 2B



- employed version 1.0 sgRNA design

FIG. 2A

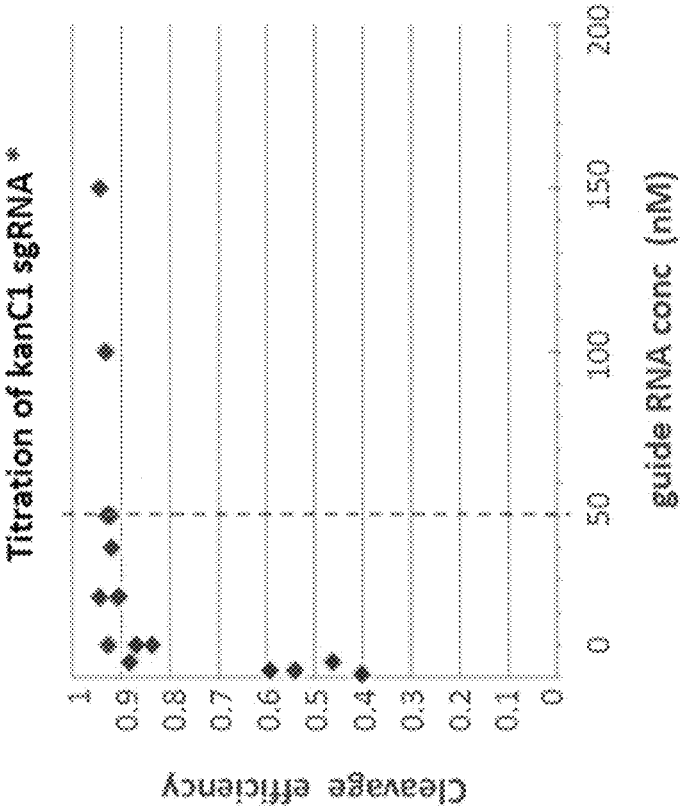

Titration of kanC1 sgRNA *
Cleavage efficiency
guide RNA conc (nM)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
50
100
150
200

FIG. 2D

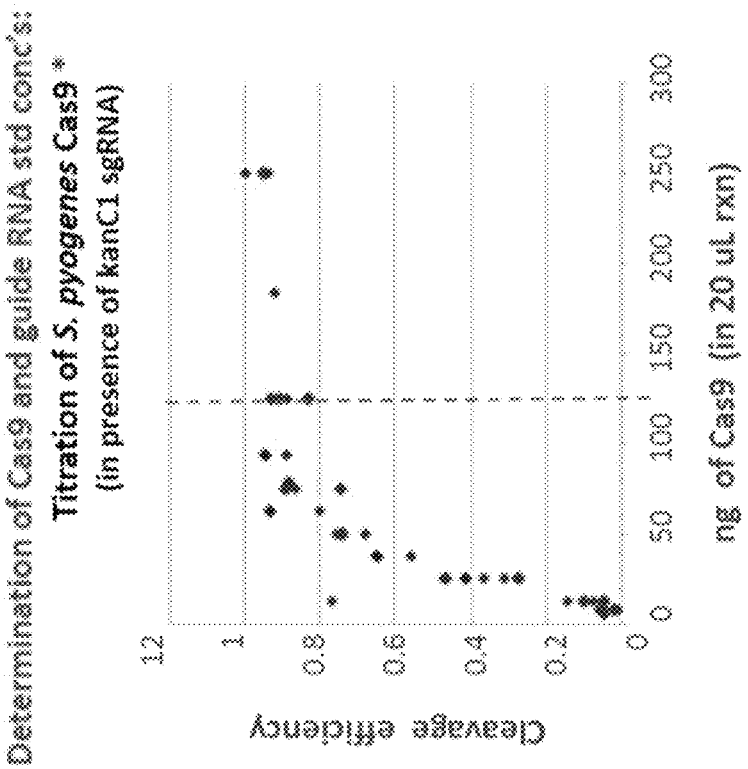

Determination of Cas9 and guide RNA std conc's:
Titration of S. pyogenes Cas9 *
(in presence of kanC1 sgRNA)
Cleavage efficiency
ng of Cas9 (in 20 uL rxn)
0
0.2
0.4
0.6
0.8
1
1.2
0
50
100
150
200
250
300

FIG. 2C

Standard cleavage conditions:

stock	volume (uL)	conc.	stoich.
10x buffer	2.0	1x	
125 ng/uL Cas9 wt protein	1.0	40 nM	16
1 uM guide RNA	1.0	50 nM	20
25 ng/uL linearized CLTA target	4.0	2.5 nM	1
ddH2O (DEPC-treated)	12.0		
	20.0		

if every ng of Cas9 in our protein prep were active

In a pre-warmed SureCycler:

(i) incubate at 37 °C for 30 min

(ii) + RNase cocktail, incubate at 37 °C for 5 min, then at 70 °C for 15 min

(iii) + Proteinase K, incubate at 37 °C for 15 min

Analyze crude products on Bioanalyzer.

FIG. 3

TABLE 1

Name of synthetic guide RNA	SEQ ID NO	Length (nt)	% Cleaved target *in vitro*	Sequence (5' → 3')
Chemical modifications tolerated by Cas9				
CLTA1 (unmodified control)	42	113	95%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
2xOMePACE_CLTA1	91	113	95%	A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAAC AGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAA GUGGCACCGAGUCGGUGCUUUUUUU
4xOMePACE_CLTA1	93	113	88%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUU*U*U*U*U
CLTA1_4xOMePACE	95	113	91%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUU*U*U*U*U
CLTA1_5xOMePACE	96	113	91%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUU*U*U*U*U
CLTA1_2'OMe+20	67	113	93%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CLTA1_2'OMe+19	68	113	93%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CLTA1_2'OMe+18	69	113	91%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CLTA1_2'OMe+17	70	113	93%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU

FIG. 4

CLTA1_2'OMe+17,18	71	113	90%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CLTA1_20_Deoxy	131	113	7%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CLTA1_20_2'OMe	74	113	89%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CLTA1_37_2'OMe	76	113	88%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CTLA1_5'SS	63	113	96%	AsGsUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAACAG CAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGU GGCACCGAGUCGGUGCUUUUUUU
CTLA1_5'SSS	64	113	94%	AsGsUsCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAAC GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAG UGGCACCGAGUCGGUGCUUUUUUU
CTLA1_5'SSSS	65	113	100%	AsGsUsCsCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAAC AGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAA GUGGCACCGAGUCGGUGCUUUUUUU
CTLA1_3'SSSS	66	113	94%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUsUsUsUsU
3xOMe_CLTA1_3xOMe	72	113	89%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
3xOMeThio_CLTA1_3xOMeThio	107	113	92%	AsGsUsCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACA GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAG UGGCACCGAGUCGGUGCUUUUsUsUsU
3xOMeThioPACE_CLTA1_3x2'OMeThioPACE	110	113	89%	A*sG*sU*sCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUA ACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAA AAGUGGCACCGAGUCGGUGCUUUUU*sU*sU*sU

FIG. 4 (cont.)

CLTA1_ZZ_70,71	122	113	19%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUZZGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU
CLTA1 ZZ_95,96	132	113	93%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CANNGAGUCGGUGCUUUUUUU
CLTA1_QB3+GNRA_DMT-ON	55	113	93%	(dmt) AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAA CAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAA AGUGGCACCGAGUCGGUGCUUUUUUU
Chemical modifications NOT tolerated by Cas9				
CLTA1_37_Deoxy	133	113	0%	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGG CACCGAGUCGGUGCUUUUUUU

LEGEND

N* = 2'OMe,3'PACE modification of nucleotide N

N*s = 2'OMe,3'thioPACE modification of nucleotide N

N = 2'OMe modification of nucleotide N

N = 2'deoxyribonucleotide N

NsN = phosphorothioate linkage noted by s

Z = Z nucleotide

dmt = dimethoxytrityl

FIG. 4 (cont.)

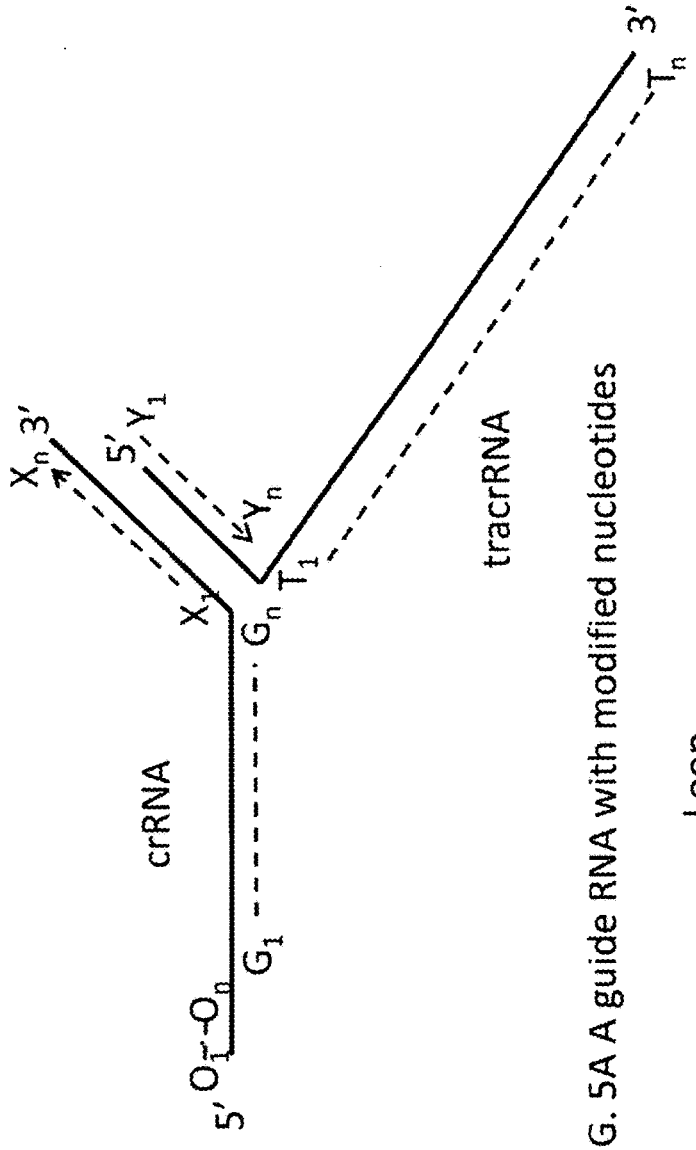


FIG. 5A A guide RNA with modified nucleotides

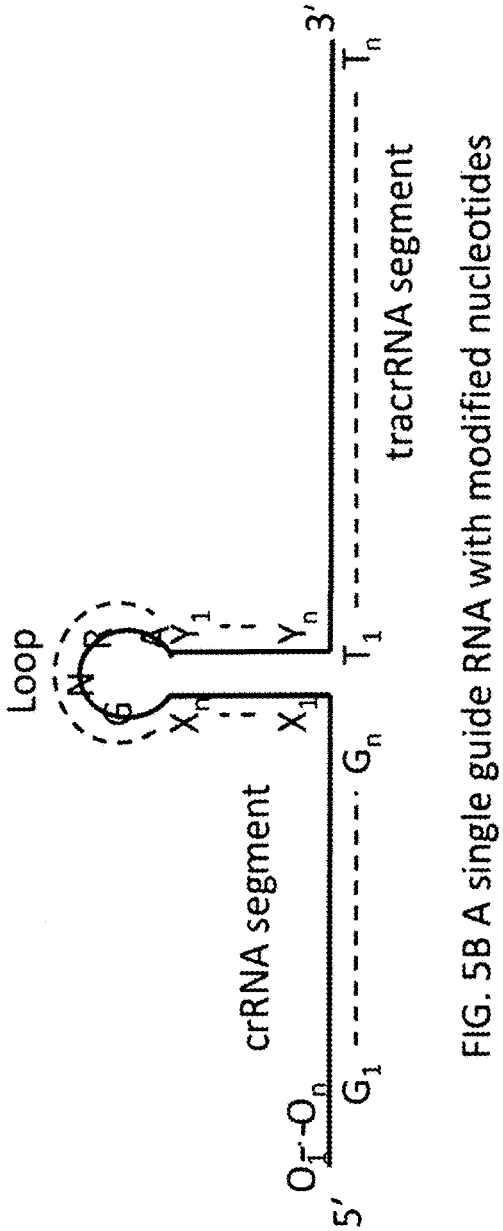
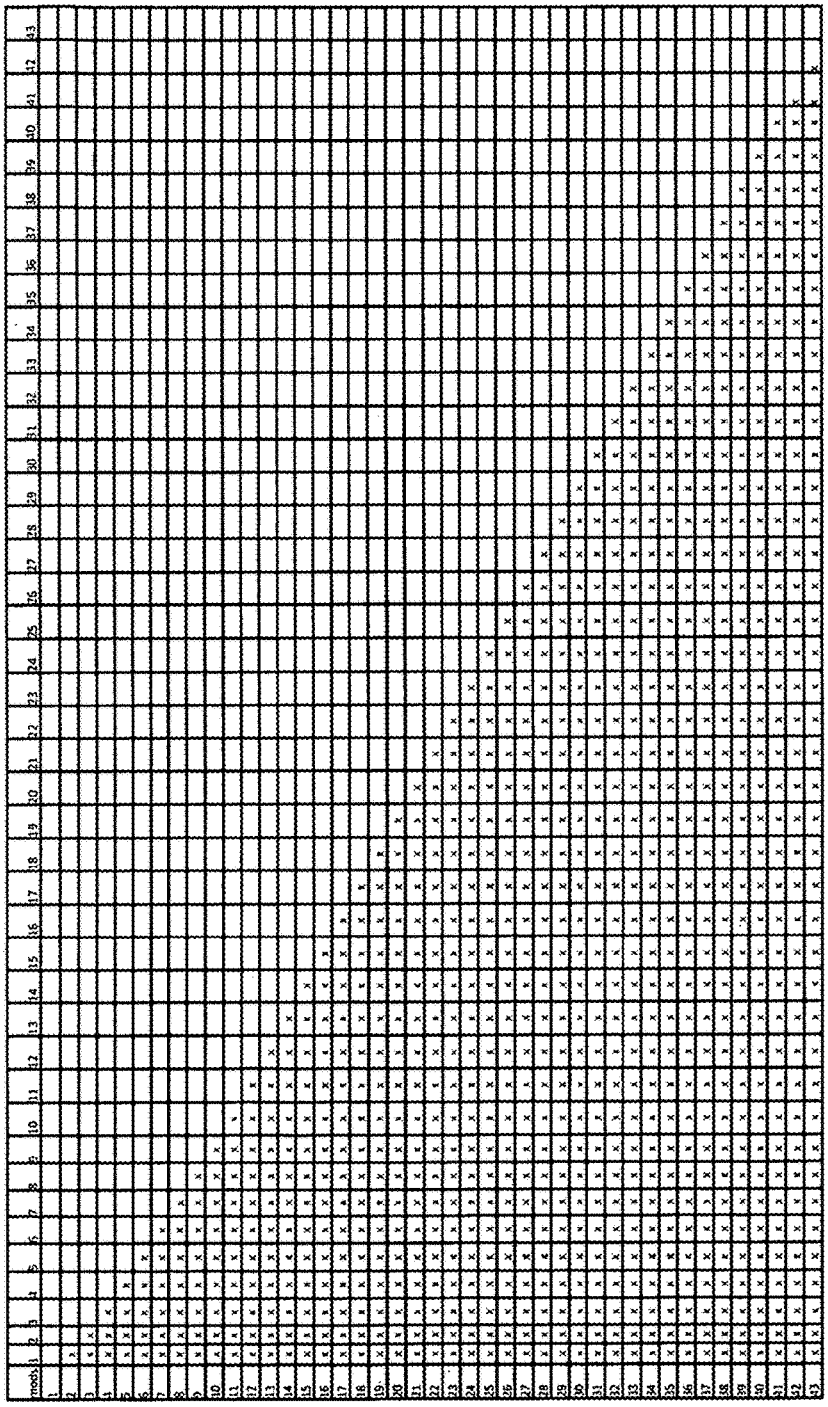


FIG. 5B A single guide RNA with modified nucleotides



1. 2'-OMe
2. 2'-H
3. 2'-MOE analog
4. 2'-fluoro analog
5. 2'-amino analog
6. 2'-arabino analog
7. 2'-F-arabino analog
8. 2'-LNA analog
9. 2'-ULNA analog
10. 4'-thioribosyl moiety
11. O-P(S) linkage
12. PACE linkage
13. thioPACE linkage
14. MethylPhosphonate
15. Boranophosphonate
16. Phosphorodithioate
17. 2-thio(U/C)
18. 4-thiouracil
19. 6-thioguanine
20. 2-aminoadenine
21. 2-aminopurine
22. pseudouracil
23. Hypoxanthine
24. 7-deaza(A/G)
25. 7-deaza-8-aza(A/G)
26. 5-methyl (U/C)
27. 5-hydroxymethyl (U/C)
28. 5,6-dehydrouracil
29. 5-propynyl (U/C)
30. 5-ethynyl (U/C)
31. 5-allyl (U/C)
32. 5-aminoallyl (U/C)
33. 5-methyl-2-pyrimidine
34. Z / P bases
35. UNA
36. x (A/G/C/T)
37. y (A/G/C/T)
38. Iso(C/G)
39. Abasic nucleotide
40. PEG
41. Hydrocarbon spacer
42. Linker-dye
43. Spermine-modification

FIG. 6

Single mod / Double mod	Sugar	Phosphorus Linkage	Base modification*	Other
Sugar/Sugar	X	X	X	X
Sugar/ P link	X	X	X	X
Sugar/Base	X	X	X	X
Sugar/other	X	X	X	X
P link/ Plink	X	X	X	X
P link/ base	X	X	X	X
P link/other	X	X	X	X
Base/ Base	X	X	X	X
Base/other	X	X	X	X
other/other	X	X	X	X

*Base modifications includes Base Pair Modifications

Sugar modifications ("Sugar"): 2'-O-Methyl (=2'-OMe) (2'-OC_1-C_4 alkyl), 2'-H, 2'-MOE (2'- OC_1-C_3 alkyl-OC_1-C_3 alkyl), 2'-F, 2'-amino, 2'-arabino, 2'-F-arabino, 2'-LNA, 2'-UNLA, 4'-thioribosyl nucleotide.
Internucleotide linkage and 3' and/or 5' terminal nucleotide modifications ("Phosphorus Linkage" or "P link"): -P(S) (phosphorothioate), -PACE (phosphonoacetate, phosphonocarboxylate), -thioPACE (thiophosphonoacetate, thiophosphonocarboxylate), -P(CH_3) (methylphosphonate, alkylphosphonate), -P(BH_3) (boranophosphonate), -P($S)_2$ (phosphorodithioate)
Base modifications: 2-thiouracil, 2-thiocytosine, 4-thiouracil, 6-thioguanine, 2-aminoadenine, 2-aminopurine, pseudouracil, hypoxanthine, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-methylcytosine, 5-methyluracil, 5-hydroxymethylcytosine,5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil,5-allyluracil, 5-allylcytosine, 5-aminoallyl-uracil, 5-aminoallyl-cytosine and abasic nucleotides.
Base Pair modifications: Z/P nucleotides, UNA, isoC/isoG, 6-thioG/5-methyl-pyrimidine, x(A,G,C,T) and y(A,G,C,T).
Other: End modifications and/or spacer/linker (ends or internal) modifications: PEG, hydrocarbon spacer, (including: heteroatom (O,S,N)-substituted hydrocarbon spacers, halo-substituted-hydrocarbon spacers, (keto,carboxy,amido,thionyl,carbamoyl,thionocarbamaoyl)-containing hydrocarbon spacers), spermine, dyes linkers including: 6-Fluorescein-phosphoramidite and the like, squarate conjugation, Diels-Alder conjugation, or "Click" chemistry conjugation.

FIG. 7

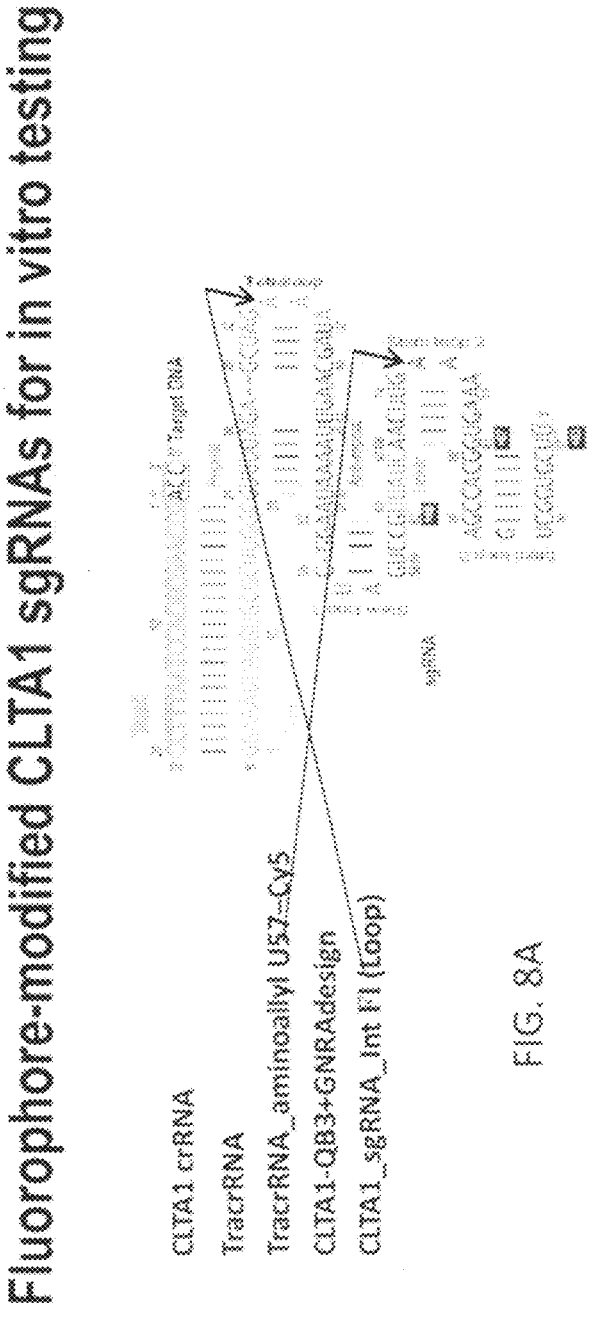

Fluorophore-modified CLTA1 sgRNAs for in vitro testing
CLTA1 crRNA
TracrRNA
TracrRNA_aminoallyl U52–Cy5
CLTA1-QB3+GNRAdesign
CLTA1_sgRNA_Int F1 (Loop)

FIG. 8A

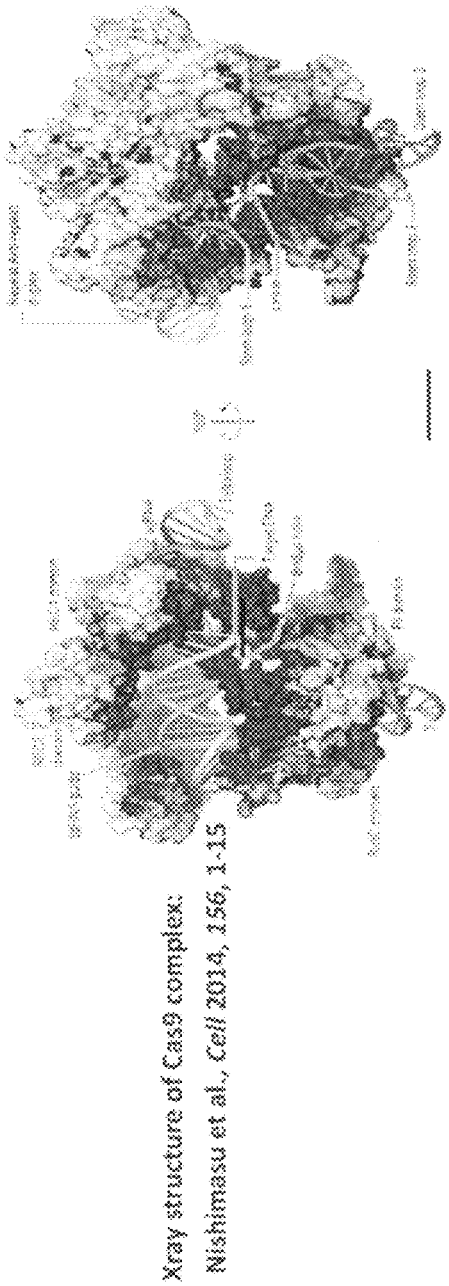

Xray structure of Cas9 complex:
Nishimasu et al., Cell 2014, 156, 1-15

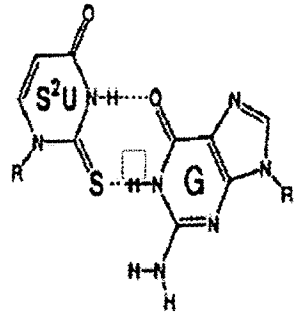
FIG. 8B

Using chemical modifications to improve specificity

Target Name	CLTA1 On- or Off-Target Site	Genomic Coordinates	COSMID Score	MIT Design Score
CLTA1 ON1	AGTCCTCATCTCCCTCAAGCAGG TCAGGAGTAGAGGGAGTTCGTCC	Chr9:36211735-36211757	0	100.0
CLTA1 OFF1	AGTCCTCAACTCCCTCAAGCAGG TCAGGAGTTGAGGGAGTTCGTCC	Chr8:15688928-15688950	0.35	61.1
CLTA1 OFF2	AGCCCTCATTTCCCTCAAGCAGG TCGGGAGTAAAGGGAGTTCGTCC	Chr3:54189084-54189106	0.65	6.4
CLTA1 OFF3	ACTCCTCATCCCCCTCAAGCCGG TGAGGAGTAGGGGGAGTTCGGCC	Chr15:88845439-88845461	0.83	4.5

Example:

- CLTA1_2thioU+11 crRNA: 5′ AGUCCUCAUC (2sU) CCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGA AUGGUCCCAAAAC 3′
- CLTA1_2thioU+9
- CLTA1_2thioU+3



Sulfur in 2-thioU cannot H-bond with G to form a wobble pair that lowers specificity.

FIG. 9A

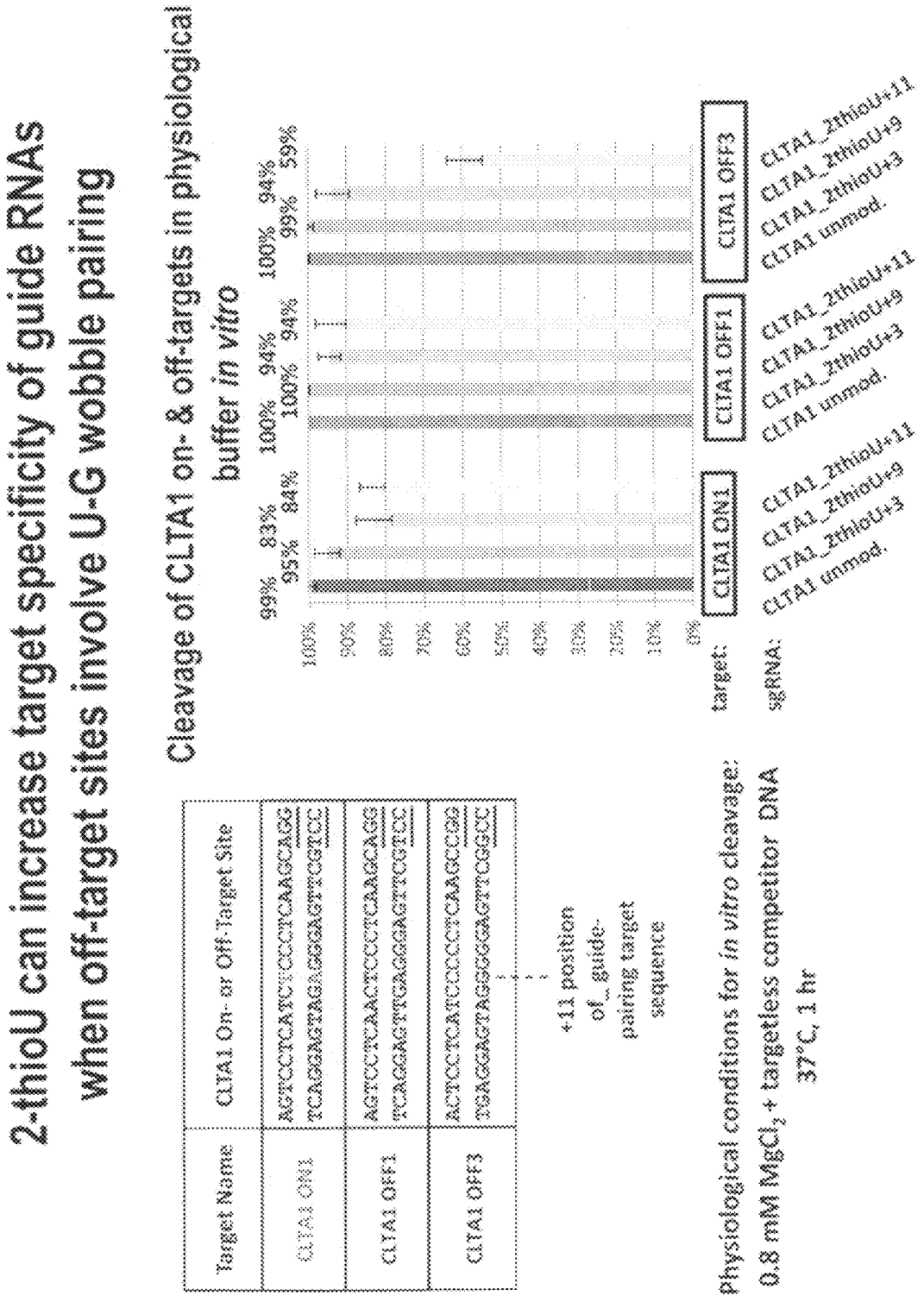

2-thioU can increase target specificity of guide RNAs when off-target sites involve U-G wobble pairing
Target Name
CLTA1 On- or Off-Target Site
CLTA1 ON1
AGTCCTCATCTCCCTCAAGCAGG
TCAGGAGTAGAGGGAGTTCGTCC
CLTA1 OFF1
AGTCCTCAACTCCCTCAAGCAGG
TCAGGAGTTGAGGGAGTTCGTCC
CLTA1 OFF3
ACTCCTCATCCCCCTCAAGCCGG
TGAGGAGTAGGGGGAGTTCGGCC
+11 position of_guide-pairing target sequence
Cleavage of CLTA1 on- & off-targets in physiological buffer in vitro
99% 83% 100% 94% 100% 94%
95% 84% 100% 94% 99% 59%
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
target:
CLTA1 ON1
CLTA1 OFF1
CLTA1 OFF3
sgRNA:
CLTA1_2thioU+11
CLTA1_2thioU+9
CLTA1_2thioU+3
CLTA1 unmod.
Physiological conditions for in vitro cleavage:
0.8 mM MgCl2 + targetless competitor DNA
37°C, 1 hr

FIG. 9B

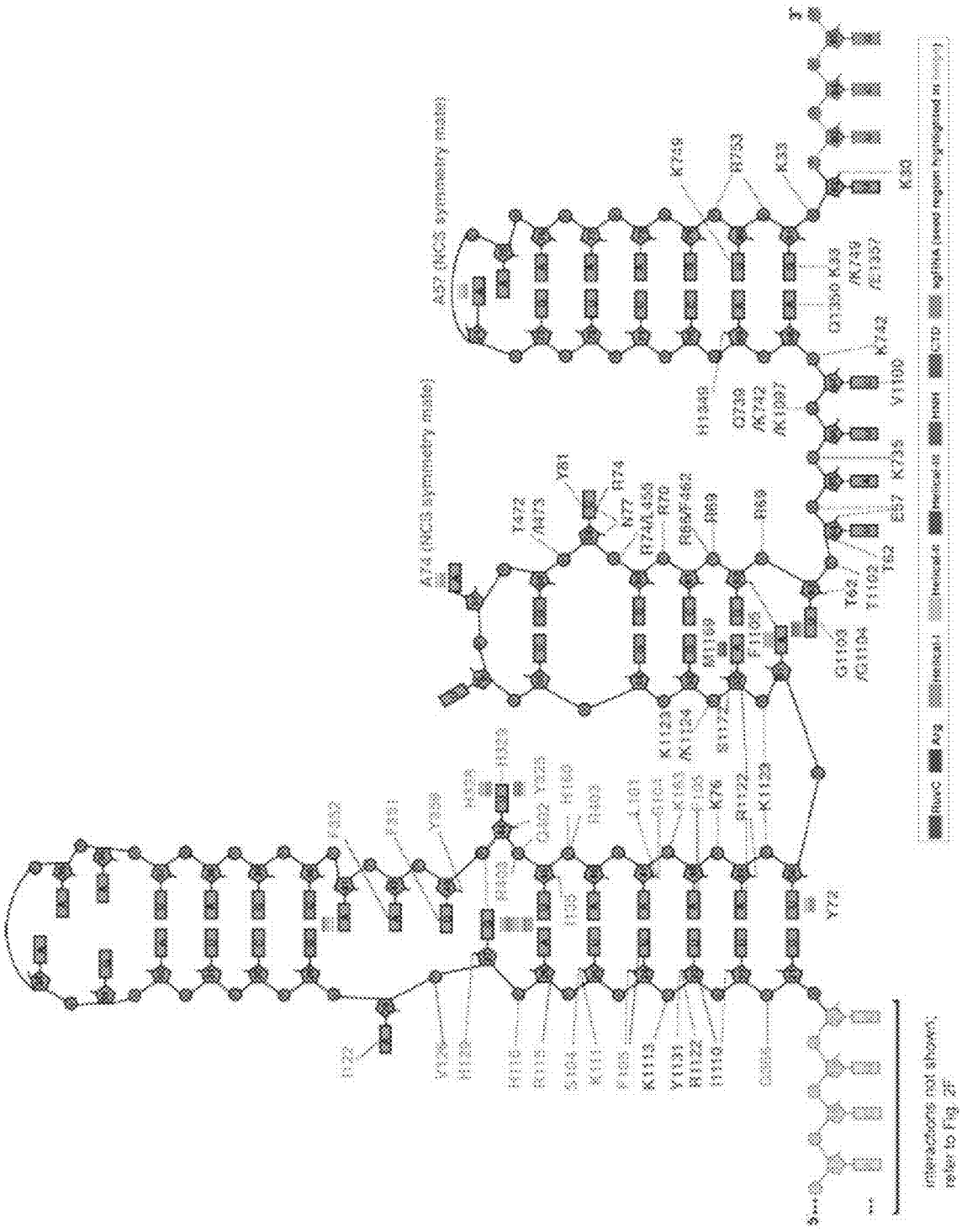


FIG. 10

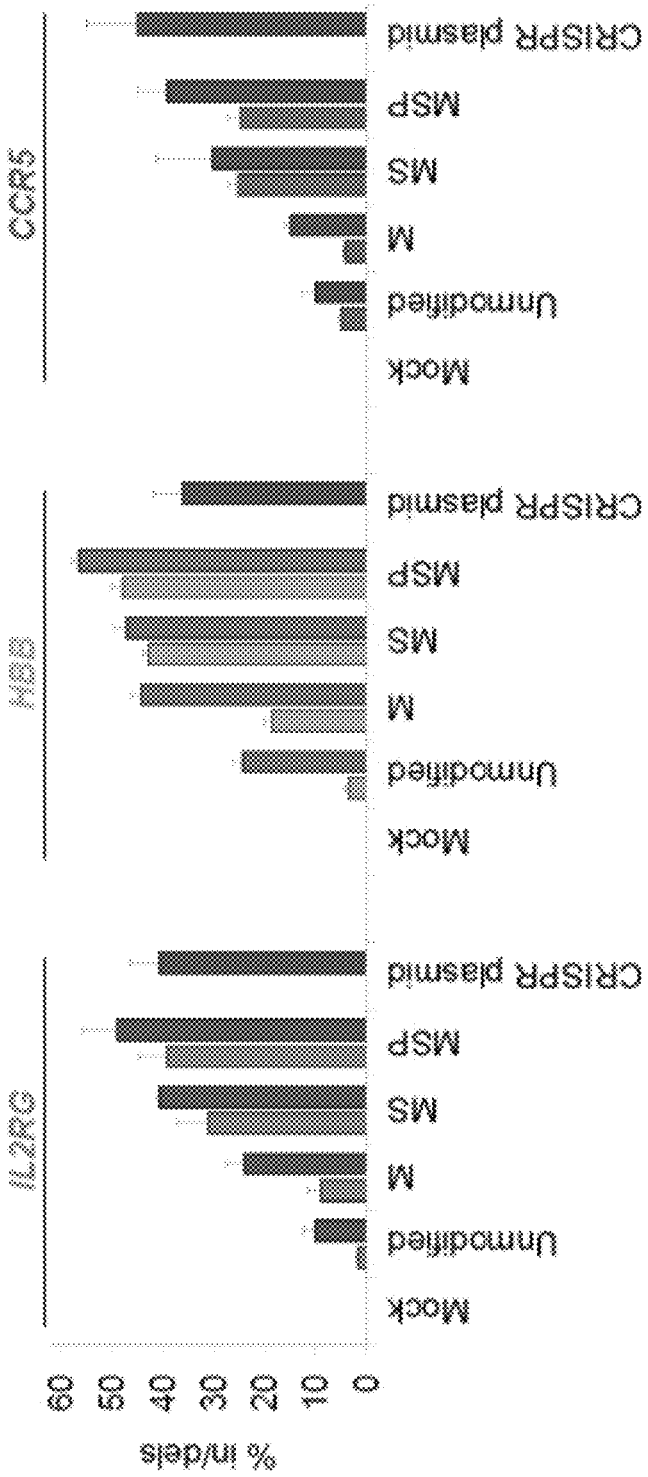

CCR5
HBB
IL2RG
Mock
Unmodified
M
MS
MSP
CRISPR plasmid
0
10
20
30
40
50
60
% In/dels

FIG. 11A

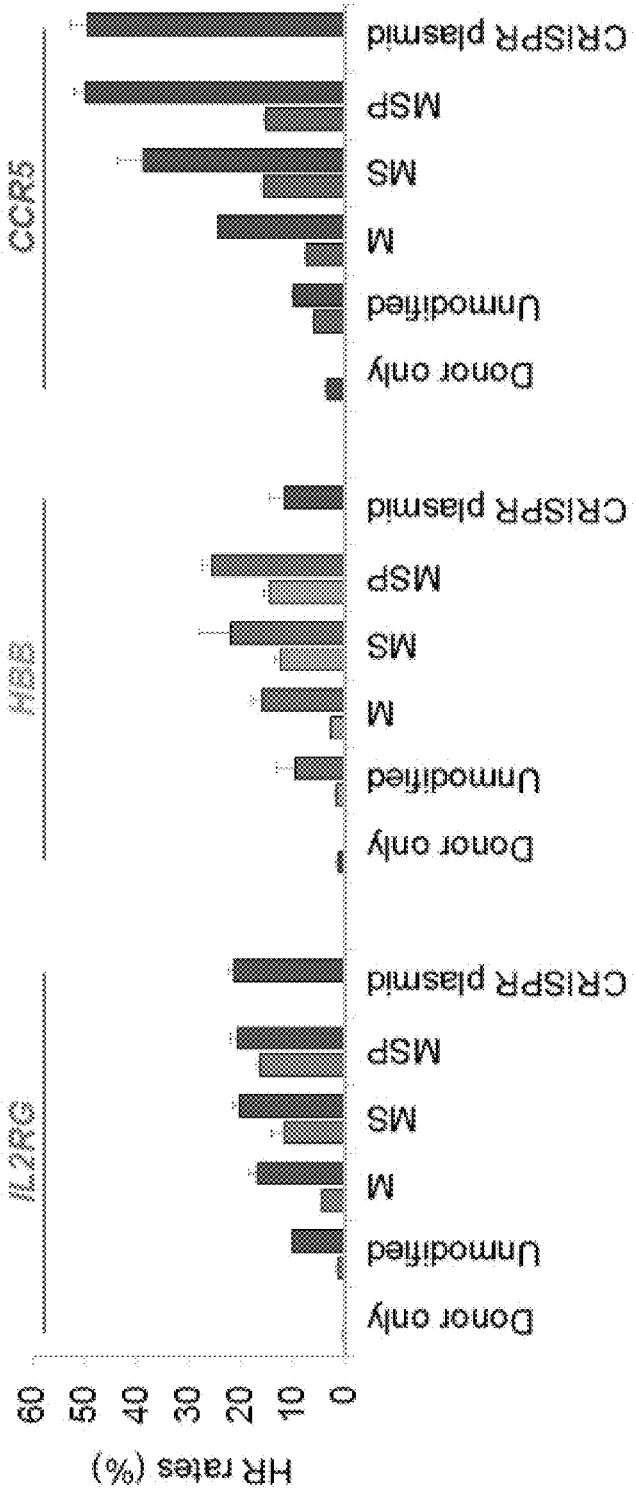

HR rates (%)
0
10
20
30
40
50
60
IL2RG
CCR5
HBB
Donor only
Unmodified
M
MS
MSP
CRISPR plasmid

FIG. 11B

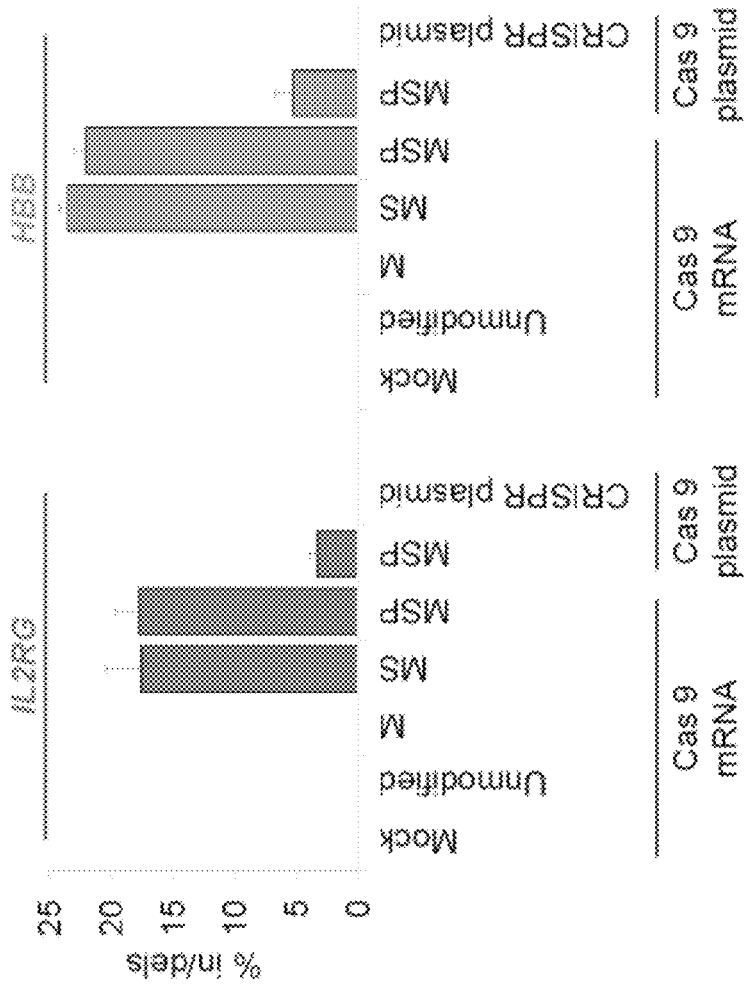


FIG. 12C

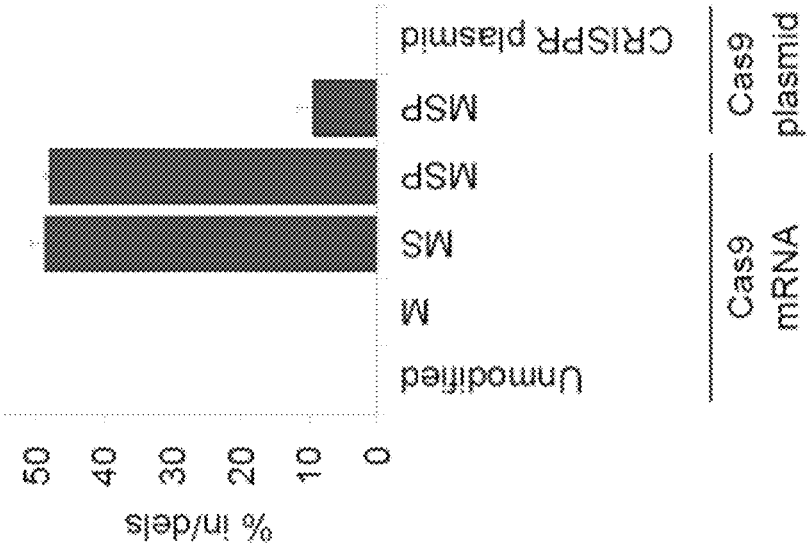


FIG. 12A

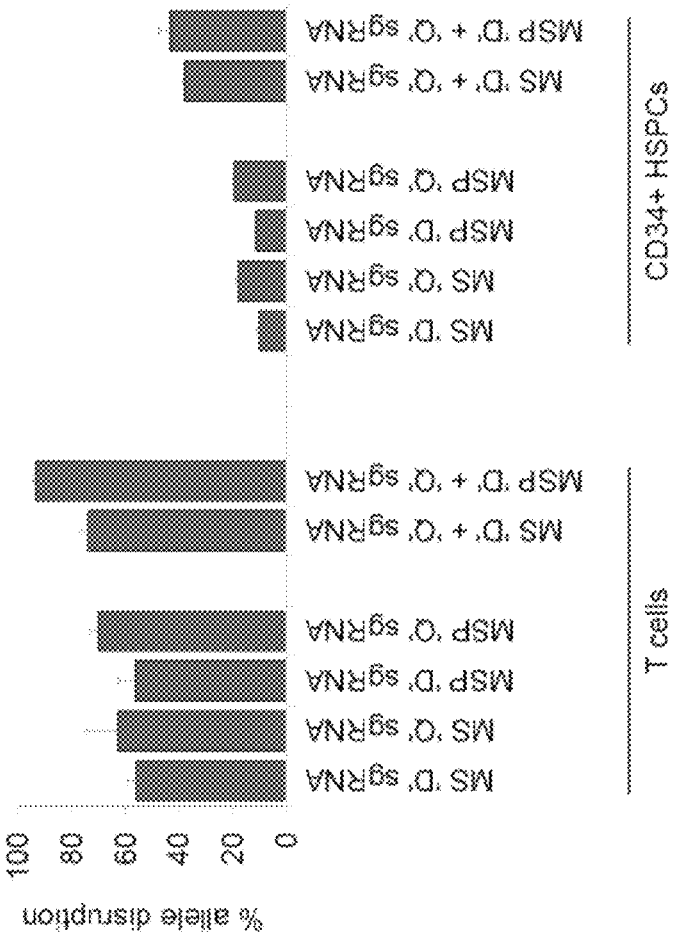


FIG. 12D

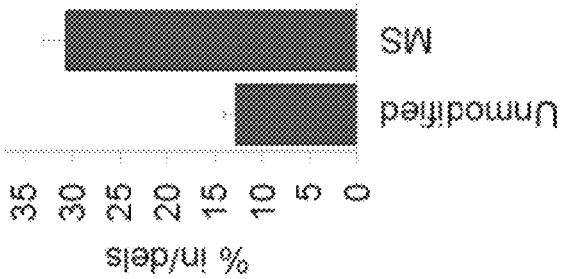


FIG. 12B

GUIDE RNA WITH CHEMICAL MODIFICATIONS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 62/256,095, filed Nov. 16, 2015, U.S. Provisional Application No. 62/146,189, filed Apr. 10, 2015, and U.S. Provisional Application No. 62/087,211, filed Dec. 3, 2014, the contents of each of which is incorporated by reference in its entirety.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Aug. 5, 2020, is named 20160013_ 04_ SL.txt and is 114,989 bytes in size

FIELD OF THE INVENTION

The present invention relates to the field of molecular biology. In particular, the present invention relates to the clusters of regularly interspaced short palindromic repeats (CRISPR) technology.

BACKGROUND OF THE INVENTION

The native prokaryotic CRISPR-Cas system comprises an array of short repeats with intervening variable sequences of constant length (i.e., clusters of regularly interspaced short palindromic repeats, or "CRISPR"), and CRISPR-associated ("Cas") proteins. The RNA of the transcribed CRISPR array is processed by a subset of the Cas proteins into small guide RNAs, which generally have two components as discussed below. There are at least three different systems: Type I, Type II and Type III. The enzymes involved in the processing of the RNA into mature crRNA are different in the 3 systems. In the native prokaryotic system, the guide RNA ("gRNA") comprises two short, non-coding RNA species referred to as CRISPR RNA ("crRNA") and trans-acting RNA ("tracrRNA"). In an exemplary system, the gRNA forms a complex with a Cas nuclease. The gRNA:Cas nuclease complex binds a target polynucleotide sequence having a protospacer adjacent motif ("PAM") and a protospacer, which is a sequence complementary to a portion of the gRNA. The recognition and binding of the target polynucleotide by the gRNA:Cas nuclease complex induces cleavage of the target polynucleotide. The native CRISPR-Cas system functions as an immune system in prokaryotes, where gRNA:Cas nuclease complexes recognize and silence exogenous genetic elements in a manner analogous to RNAi in eukaryotic organisms, thereby conferring resistance to exogenous genetic elements such as plasmids and phages.

It has been demonstrated that a single-guide RNA ("sgRNA") can replace the complex formed between the naturally-existing crRNA and tracrRNA.

Considerations relevant to developing a gRNA, including a sgRNA, include specificity, stability, and functionality. Specificity refers to the ability of a particular gRNA:Cas nuclease complex to bind to and/or cleave a desired target sequence, whereas little or no binding and/or cleavage of polynucleotides different in sequence and/or location from the desired target occurs. Thus, specificity refers to minimizing off-target effects of the gRNA:Cas nuclease complex. Stability refers to the ability of the gRNA to resist degradation by enzymes, such as nucleases, and other substances that exist in intra-cellular and extra-cellular environments. Thus, there is a need for providing gRNA, including sgRNA, having increased resistance to nucleolytic degradation, increased binding affinity for the target polynucleotide, and/or reduced off-target effects while, nonetheless, having gRNA functionality. Further considerations relevant to developing a gRNA include transfectability and immunostimulatory properties. Thus, there is a need for providing gRNA, including sgRNA, having efficient and titratable transfectability into cells, especially into the nuclei of eukaryotic cells, and having minimal or no immunostimulatory properties in the transfected cells. Another important consideration for gRNA is to provide an effective means for delivering it into and maintaining it in the intended cell, tissue, bodily fluid or organism for a duration sufficient to allow the desired gRNA functionality.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** is a set of diagrams showing a schematic model of an exemplary CRISPR-Cas system. The exemplary system shown here is a Type II system having a Cas nuclease. In this particular example, the Cas nuclease is the Cas9 nuclease. The Cas9 nuclease recognizes a PAM sequence (here, the PAM sequence is a 3-nt sequence of NGG, where N is A, G, C or T, but other PAM sequences are known to exist). The sgRNA includes a guide sequence, a crRNA sequence or segment, and tracrRNA sequence or segment. The guide sequence of the sgRNA hybridizes with the DNA target directly upstream of the PAM sequence. In the example shown here, Cas9 mediates a double-stranded break upstream of the PAM sequence (arrows).

FIG. **2**A is a diagram showing an exemplary CRISPR-Cas9-mediated cleavage assay.

FIG. **2**B is a table showing components and their concentrations for a biochemical cleavage assay used to generate the data in FIG. **4**.

FIG. **2**C is a diagram showing titration of *Streptococcus pyogenes* Cas9 nuclease for the biochemical cleavage assay.

FIG. **2**D is a diagram showing titration of an exemplary sgRNA for the biochemical cleavage assay. In this example a sgRNA named kanC1 is targeted to a complementary sequence in the kanamycin resistance gene.

FIG. **3** shows exemplary conditions and procedures for the biochemical cleavage assay which uses purified components in vitro.

FIG. **4** is a table showing the data obtained using exemplary modified guide RNAs in the cleavage assay.

FIG. **5**A shows an exemplary guide RNA disclosed in the application.

FIG. **5**B shows an exemplary single guide RNA (sgRNA) disclosed in the application.

FIG. **6** is a table showing exemplary guide RNAs having at least two chemical modifications (e.g., a first modification and a second modification). Each number represents a modification as indicated and each "x" indicates the combination of modifications in a guide RNA. In certain embodiments, the first and second modifications are present on a single nucleotide. In certain embodiments, the first and second modifications are present on separate nucleotides.

FIG. **7** shows exemplary types of guide RNAs having at least three chemical modifications. The lower part of FIG. **7** lists several types of modifications. The table in the upper part of FIG. **7** indicates how a double modification ("double mod," a combination of two types of modifications) can be

combined with a single modification ("single mod," one type of modification). An "x" indicates the presence of the corresponding double mod and single mod in a guide RNA.

FIGS. **8**A and **8**B show fluorophore-modified CLTA1 sgRNAs for in vitro testing. In FIG. **8**A, the RNA sequence (SEQ ID NO: 135) of a sgRNA for CLTA1 is shown, including a position where a fluorescent dye or a label could be attached to the sgRNA. Target DNA is SEQ ID NO: 134. FIG. **8**B shows a structure determined by Xray crystallography of a Cas9:sgRNA complex, as reported in Nishimasu et al., *Cell* 2014, 156, 1-15.

FIG. **9**A shows CLTA1 sgRNAs modified with 2-thiouridine at certain locations (positions 3, 9 and 11) in an effort to improve specificity for the target CTLA1. Top strand and bottom strand sequences (respectively) of the CTLA1 targets are: ON1 (SEQ ID NOs: 136 and 137); OFF1 (SEQ ID NOs: 138 and 139); OFF2 (SEQ ID NOs: 140 and 141); and OFF3 (SEQ ID NOs: 142 and 143). FIG. **9**B shows that gRNA modified with 2-thioU (SEQ ID NO: ###) can increase target specificity of the gRNAs when off-target sites involve U-G wobble pairing. In particular, the CTLA1_2thioU+11 had much lower cleavage of the off-target sequence CLTA1 OFF3, which has a T to C mutation at the 11 position in the 5' strand. Top strand and bottom strand sequences (respectively) of the CTLA1 targets are: ON1 (SEQ ID NOs: 136 and 137); OFF1 (SEQ ID NOs: 138 and 139); and OFF3 (SEQ ID NOs: 142 and 143).

FIG. **10** shows the guide RNA scaffold secondary structure, displaying noncovalent binding interactions with amino acids of Cas9, as reported in Jiang et al., Science (2015) 348:6242, 1477-81.

FIGS. **11**A and **11**B illustrate experimental results showing that gene disruption in human cell lines, with high frequencies of indels and homologous recombination (HR), can be achieved using synthesized and chemically modified sgRNAs disclosed herein, as reported in Hendel et al., *Nat. Biotechnol.* (2015) 33:9, 985-9.

FIGS. **12**A, **12**B, **12**C and **12**D illustrate experimental results showing that chemically modified sgRNAs as described herein can be used to achieve high frequencies of gene disruption or targeted genome editing in stimulated primary human T cells as well as in CD34+ hematopoietic stem and progenitor cells (HSPCs), as reported in Hendel et al., *Nat. Biotechnol.* (2015) 33:9, 985-9.

DETAILED DESCRIPTION OF THE INVENTION

This invention is based, at least in part, on an unexpected discovery that certain chemical modifications to gRNA are tolerated by the CRISPR-Cas system. In particular, certain chemical modifications believed to increase the stability of the gRNA, to alter the thermostability of a gRNA hybridization interaction, and/or to decrease the off-target effects of Cas:gRNA complexation do not substantially compromise the efficacy of Cas:gRNA binding to, nicking of, and/or cleavage of the target polynucleotide. Furthermore, certain chemical modifications are believed to provide gRNA, including sgRNA, having efficient and titratable transfectability into cells, especially into the nuclei of eukaryotic cells, and/or having minimal or no immunostimulatory properties in the transfected cells. Certain chemical modifications are believed to provide gRNA, including sgRNA, which can be effectively delivered into and maintained in the intended cell, tissue, bodily fluid or organism for a duration sufficient to allow the desired gRNA functionality.

I. Definitions

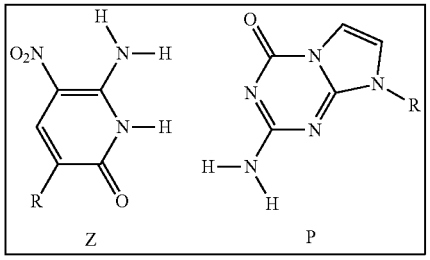
As used herein, the term "guide RNA" generally refers to an RNA molecule (or a group of RNA molecules collectively) that can bind to a Cas protein and aid in targeting the Cas protein to a specific location within a target polynucleotide (e.g., a DNA). A guide RNA can comprise a crRNA segment and a tracrRNA segment. As used herein, the term "crRNA" or "crRNA segment" refers to an RNA molecule or portion thereof that includes a polynucleotide-targeting guide sequence, a stem sequence, and, optionally, a 5'-overhang sequence. As used herein, the term "tracrRNA" or "tracrRNA segment" refers to an RNA molecule or portion thereof that includes a protein-binding segment (e.g., the protein-binding segment is capable of interacting with a CRISPR-associated protein, such as a Cas9). The term "guide RNA" encompasses a single guide RNA (sgRNA), where the crRNA segment and the tracrRNA segment are located in the same RNA molecule. The term "guide RNA" also encompasses, collectively, a group of two or more RNA molecules, where the crRNA segment and the tracrRNA segment are located in separate RNA molecules.

The term "scaffold" refers to the portions of guide RNA molecules comprising sequences which are substantially identical or are highly conserved across natural biological species. Scaffolds include the tracrRNA segment and the portion of the crRNA segment other than the polynucleotide-targeting guide sequence at or near the 5' end of the crRNA segment, excluding any unnatural portions comprising sequences not conserved in native crRNAs and tracrRNAs.

The term "nucleic acid", "polynucleotide" or "oligonucleotide" refers to a DNA molecule, an RNA molecule, or analogs thereof. As used herein, the terms "nucleic acid", "polynucleotide" and "oligonucleotide" include, but are not limited to DNA molecules such as cDNA, genomic DNA or synthetic DNA and RNA molecules such as a guide RNA, messenger RNA or synthetic RNA. Moreover, as used herein, the terms "nucleic acid" and "polynucleotide" include single-stranded and double-stranded forms.

The term "modification" in the context of an oligonucleotide or polynucleotide includes but is not limited to (a) end modifications, e.g., 5' end modifications or 3' end modifications, (b) nucleobase (or "base") modifications, including replacement or removal of bases, (c) sugar modifications, including modifications at the 2', 3', and/or 4' positions, and (d) backbone modifications, including modification or replacement of the phosphodiester linkages. The term "modified nucleotide" generally refers to a nucleotide having a modification to the chemical structure of one or more of the base, the sugar, and the phosphodiester linkage or backbone portions, including nucleotide phosphates.

The terms "Z" and "P" refer to the nucleotides, nucleobases, or nucleobase analogs developed by Steven Benner and colleagues as described for example in "Artificially expanded genetic information system: a new base pair with an alternative hydrogen bonding pattern" Yang, Z., Hutter, D., Sheng, P., Sismour, A. M. and Benner, S. A. (2006) *Nucleic Acids Res.*, 34, 6095-101, the contents of which is hereby incorporated by reference in its entirety.



The terms "xA", "xG", "xC", "xT", or "x(A,G,C,T)" and "yA", "yG", "yC", "yT", or "y(A,G,C,T)" refer to nucleotides, nucleobases, or nucleobase analogs as described by Krueger et al in "Synthesis and Properties of Size-Expanded DNAs: Toward Designed, Functional Genetic Systems"; Andrew T. Krueger, Haige Lu, Alex H. F. Lee, and Eric T. Kool (2007) *Acc. Chem. Res.*, 40, 141-50, the contents of which is hereby incorporated by reference in its entirety.

The term "Unstructured Nucleic Acid" or "UNA" refers to nucleotides, nucleobases, or nucleobase analogs as described in U.S. Pat. No. 7,371,580, the contents of which is hereby incorporated by reference in its entirety. An unstructured nucleic acid, or UNA, modification is also referred to as a "pseudo-complementary" nucleotide, nucleobase or nucleobase analog (see e.g., Lahoud et al. (1991) *Nucl. Acids Res.*, 36:10, 3409-19).

The terms "PACE" and "thioPACE" refer to internucleotide phosphodiester linkage analogs containing phosphonoacetate or thiophosphonoacetate groups, respectively. These modifications belong to a broad class of compounds comprising phosphonocarboxylate moiety, phosphonocarboxylate ester moiety, thiophosphonocarboxylate moiety and thiophosphonocarboxylate ester moiety. These linkages can be described respectively by the general formulae $P(CR_1R_2)_nCOOR$ and $(S)—P(CR_1R_2)_nCOOR$ wherein n is an integer from 0 to 6 and each of R_1 and R_2 is independently selected from the group consisting of H, an alkyl and substituted alkyl. Some of these modifications are described by Yamada et al. in "Synthesis and Biochemical Evaluation of Phosphonoformate Oligodeoxyribonucleotides" Christina M. Yamada, Douglas J. Dellinger and Marvin H. Caruthers (2006) *J. Am. Chem. Soc.* 128:15, 5251-61, the contents of which is hereby incorporated by reference in its entirety.

As used herein, "modification" refers to a chemical moiety, or portion of a chemical structure, which differs from that found in unmodified ribonucleotides, namely adenosine, guanosine, cytidine, and uridine ribonucleotides. The term "modification" may refer to type of modification. For example, "same modification" means same type of modification, and "the modified nucleotides are the same" means the modified nucleotides have the same type(s) of modification while the base (A, G, C, U, etc.) may be different. Similarly, a guide RNA with "two modifications" is a guide RNA with two types of modifications, which may or may not be in the same nucleotide, and each type may appear in multiple nucleotides in the guide RNA. Similarly, a guide RNA with "three modifications" is a guide RNA with three types of modifications, which may or may not be in the same nucleotide, and each type may appear in multiple nucleotides.

As used herein, the term "target polynucleotide" or "target" refers to a polynucleotide containing a target nucleic acid sequence. A target polynucleotide may be single-stranded or double-stranded, and, in certain embodiments, is double-stranded DNA. In certain embodiments, the target polynucleotide is single-stranded RNA. A "target nucleic acid sequence" or "target sequence," as used herein, means a specific sequence or the complement thereof that one wishes to bind to, nick, or cleave using a CRISPR system.

The term "hybridization" or "hybridizing" refers to a process where completely or partially complementary polynucleotide strands come together under suitable hybridization conditions to form a double-stranded structure or region in which the two constituent strands are joined by hydrogen bonds. As used herein, the term "partial hybridization" includes where the double-stranded structure or region contains one or more bulges or mismatches. Although hydrogen bonds typically form between adenine and thymine or adenine and uracil (A and T or A and U) or cytosine and guanine (C and G), other noncanonical base pairs may form (See e.g., Adams et al., "The Biochemistry of the Nucleic Acids," 11th ed., 1992). It is contemplated that modified nucleotides may form hydrogen bonds that allow or promote hybridization.

The term "cleavage" or "cleaving" refers to breaking of the covalent phosphodiester linkage in the ribosylphosphodiester backbone of a polynucleotide. The terms "cleavage" or "cleaving" encompass both single-stranded breaks and double-stranded breaks. Double-stranded cleavage can occur as a result of two distinct single-stranded cleavage events. Cleavage can result in the production of either blunt ends or staggered ends.

The term "CRISPR-associated protein" or "Cas protein" refers to a wild type Cas protein, a fragment thereof, or a mutant or variant thereof. The term "Cas mutant" or "Cas variant" refers to a protein or polypeptide derivative of a wild type Cas protein, e.g., a protein having one or more point mutations, insertions, deletions, truncations, a fusion protein, or a combination thereof. In certain embodiments, the "Cas mutant" or "Cas variant" substantially retains the nuclease activity of the Cas protein. In certain embodiments, the "Cas mutant" or "Cas variant" is mutated such that one or both nuclease domains are inactive. In certain embodiments, the "Cas mutant" or "Cas variant" has nuclease activity. In certain embodiments, the "Cas mutant" or "Cas variant" lacks some or all of the nuclease activity of its wild-type counterpart.

The term "nuclease domain" of a Cas protein refers to the polypeptide sequence or domain within the protein which possesses the catalytic activity for DNA cleavage. A nuclease domain can be contained in a single polypeptide chain, or cleavage activity can result from the association of two (or more) polypeptides. A single nuclease domain may consist of more than one isolated stretch of amino acids within a given polypeptide. Examples of these domains include RuvC-like motifs (amino acids 7-22, 759-766 and 982-989 in SEQ ID NO: 1) and HNH motif (aa 837-863). See Gasiunas et al. (2012) *Proc. Natl. Acad. Sci. USA*, 109:39, E2579-E2586 and WO2013176772.

A synthetic guide RNA that has "gRNA functionality" is one that has one or more of the functions of naturally occurring guide RNA, such as associating with a Cas protein, or a function performed by the guide RNA in association with a Cas protein. In certain embodiments, the functionality includes binding a target polynucleotide. In certain embodiments, the functionality includes targeting a Cas protein or a gRNA:Cas protein complex to a target polynucleotide. In certain embodiments, the functionality includes nicking a target polynucleotide. In certain embodiments, the functionality includes cleaving a target polynucleotide. In certain embodiments, the functionality

includes associating with or binding to a Cas protein. In certain embodiments, the functionality is any other known function of a guide RNA in a CRISPR-Cas system with a Cas protein, including an artificial CRISPR-Cas system with an engineered Cas protein. In certain embodiments, the functionality is any other function of natural guide RNA. The synthetic guide RNA may have gRNA functionality to a greater or lesser extent than a naturally occurring guide RNA. In certain embodiments, a synthetic guide RNA may have greater functionality as to one property and lesser functionality as to another property in comparison to a similar naturally occurring guide RNA.

A "Cas protein having a single-strand nicking activity" refers to a Cas protein, including a Cas mutant or Cas variant, that has reduced ability to cleave one of two strands of a dsDNA as compared to a wild type Cas protein. For example, in certain embodiments, a Cas protein having a single-strand nicking activity has a mutation (e.g., amino acid substitution) that reduces the function of the RuvC domain (or the HNH domain) and as a result reduces the ability to cleave one strand of the target DNA. Examples of such variants include the D10A, H839A/H840A, and/or N863A substitutions in *S. pyogenes* Cas9, and also include the same or similar substitutions at equivalent sites in Cas9 enzymes of other species.

As used herein, the term "portion" or "fragment" of a sequence refers to any portion of the sequence (e.g., a nucleotide subsequence or an amino acid subsequence) that is smaller than the complete sequence. Portions of polynucleotides can be any length, for example, at least 5, 10, 15, 20, 25, 30, 40, 50, 75, 100, 150, 200, 300 or 500 or more nucleotides in length. A portion of a guide sequence can be about 50%, 40%, 30%, 20%, 10% of the guide sequence, e.g., one-third of the guide sequence or shorter, e.g., 7, 6, 5, 4, 3, or 2 nucleotides in length.

The term "derived from" in the context of a molecule refers to a molecule isolated or made using a parent molecule or information from that parent molecule. For example, a Cas9 single mutant nickase and a Cas9 double mutant null-nuclease are derived from a wild-type Cas9 protein.

The term "substantially identical" in the context of two or more polynucleotides (or two or more polypeptides) refers to sequences or subsequences that have at least about 60%, at least about 70%, at least about 80%, at least about 90%, about 90-95%, at least about 95%, at least about 98%, at least about 99% or more nucleotide (or amino acid) sequence identity, when compared and aligned for maximum correspondence using a sequence comparison algorithm or by visual inspection. Preferably, the "substantial identity" between polynucleotides exists over a region of the polynucleotide at least about 50 nucleotides in length, at least about 100 nucleotides in length, at least about 200 nucleotides in length, at least about 300 nucleotides in length, at least about 500 nucleotides in length, or over the entire length of the polynucleotide. Preferably, the "substantial identity" between polypeptides exists over a region of the polypeptide at least about 50 amino acid residues in length, at least about 100 amino acid residues in length, or over the entire length of the polypeptide.

As disclosed herein, a number of ranges of values are provided. It is understood that each intervening value, to the tenth of the unit of the lower limit, between the upper and lower limits of that range is also specifically contemplated. Each smaller range or intervening value encompassed by a stated range is also specifically contemplated. The term "about" generally refers to plus or minus 10% of the indicated number. For example, "about 10%" may indicate a range of 9% to 11%, and "about 20" may mean from 18-22. Other meanings of "about" may be apparent from the context, such as rounding off, so, for example "about 1" may also mean from 0.5 to 1.4.

II. CRISPR-Mediated Sequence-Specific Binding and/or Cleavage

Shown in FIG. **1** is a diagram of CRISPR-Cas9-mediated sequence-specific cleavage of DNA. The guide RNA is depicted as sgRNA with an exemplary 20-nucleotide (20-nt) guide sequence (other guide sequences may be, for example, from about 15 to about 30 nts in length) within the 5' domain, an internally positioned base-paired stem, and a 3' domain. The guide sequence is complementary to an exemplary 20-nt target sequence in a DNA target. The stem corresponds to a repeat sequence in crRNA and is complementary to a sequence in the tracrRNA. The 3' domain of the guide RNA corresponds to the 3' domain of the tracrRNA that binds a Cas9 nuclease. The Cas9:guide RNA complex binds and cleaves a target DNA sequence or protospacer directly upstream of a PAM sequence recognized by Cas9. In FIG. **1**, a 3-nt PAM sequence is exemplified; however other PAM sequences, including 4-nt and 5-nt PAM sequences are known. In the system exemplified in FIG. **1**, both strands of the target sequence in DNA are cleaved by Cas9 at the sites indicated by arrows.

III. Guide RNAs

In at least one aspect, the present invention comprises a chemically modified guide RNA that has guide RNA functionality. A guide RNA that comprises any nucleotide other than the four canonical ribonucleotides, namely A, C, G, and U, whether unnatural or natural (e.g., a pseudouridine, inosine or a deoxynucleotide), is a chemically modified guide RNA. Likewise a guide RNA that comprises any backbone or internucleotide linkage other than a natural phosphodiester internucleotide linkage possesses a chemical modification and therefore is a chemically modified guide RNA. In certain embodiments, the retained functionality includes binding a Cas protein. In certain embodiments, the retained functionality includes binding a target polynucleotide. In certain embodiments, the retained functionality includes targeting a Cas protein or a gRNA:Cas protein complex to a target polynucleotide. In certain embodiments, the retained functionality includes nicking a target polynucleotide by a gRNA:Cas protein complex. In certain embodiments, the retained functionality includes cleaving a target polynucleotide by a gRNA:Cas protein complex. In certain embodiments, the retained functionality is any other known function of a guide RNA in a CRISPR-Cas system with a Cas protein, including an artificial CRISPR-Cas system with an engineered Cas protein. In certain embodiments, the retained functionality is any other function of a natural guide RNA.

A. Exemplary Modifications

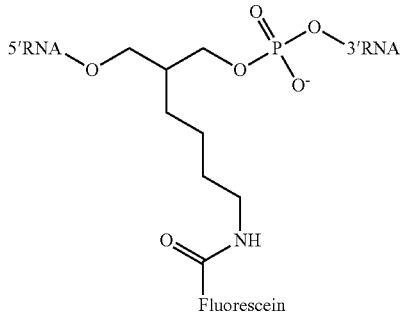
In certain embodiments, a nucleotide sugar modification incorporated into the guide RNA is selected from the group consisting of 2'-O—C_{1-4}alkyl such as 2'-O-methyl (2'-OMe), 2'-deoxy (2'-H), 2'-O—C_{1-3}alkyl-O—C_{1-3}alkyl such as 2'-methoxyethyl ("2'-MOE"), 2'-fluoro ("2'-F"), 2'-amino ("2'-NH_2"), 2'-arabinosyl ("2'-arabino") nucleotide, 2'-F-arabinosyl ("2'-F-arabino") nucleotide, 2'-locked nucleic

acid ("LNA") nucleotide, 2'-unlocked nucleic acid ("ULNA") nucleotide, a sugar in L form ("L-sugar"), and 4'-thioribosyl nucleotide. In certain embodiments, an internucleotide linkage modification incorporated into the guide RNA is selected from the group consisting of: phosphorothioate "P(S)" (P(S)), phosphonocarboxylate ($P(CH_2)_n$ COOR) such as phosphonoacetate "PACE" ($P(CH_2COO^-)$), thiophosphonocarboxylate ($(S)P(CH_2)_nCOOR$) such as thiophosphonoacetate "thioPACE" ($(S)P(CH_2COO^-)$), alkylphosphonate ($P(C_{1-3}alkyl)$ such as methylphosphonate —$P(CH_3)$, boranophosphonate ($P(BH_3)$), and phosphorodithioate ($P(S)_2$).

In certain embodiments, a nucleobase ("base") modification incorporated into the guide RNA is selected from the group consisting of: 2-thiouracil ("2-thioU"), 2-thiocytosine ("2-thioC"), 4-thiouracil ("4-thioU"), 6-thioguanine ("6-thioG"), 2-aminoadenine ("2-aminoA"), 2-aminopurine, pseudouracil, hypoxanthine, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-methylcytosine ("5-methylC"), 5-methyluracil ("5-methylU"), 5-hydroxymethylcytosine, 5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil, 5-allyluracil ("5-allylU"), 5-allylcytosine ("5-allylC"), 5-aminoallyluracil ("5-aminoallylU"), 5-aminoallyl-cytosine ("5-aminoallylC"), an abasic nucleotide, Z base, P base, Unstructured Nucleic Acid ("UNA"), isoguanine ("isoG"), isocytosine ("isoC") [as described in "Enzymatic Incorporation of a New Base pair into DNA and RNA Extends the Genetic Alphabet." Piccirilli, J. A.; Krauch, T.; Moroney, S. E.; Benner, S. A. (1990) *Nature,* 343, 33], 5-methyl-2-pyrimidine [as described in Rappaport, H. P. (1993) *Biochemistry,* 32, 3047], x(A,G,C,T) and y(A,G,C,T).

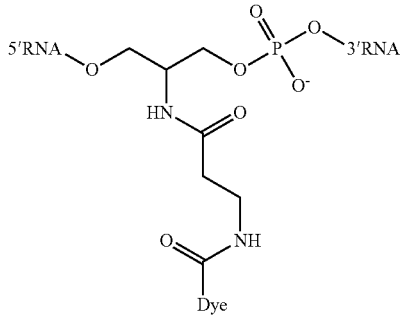
In certain embodiments, one or more isotopic modifications are introduced on the nucleotide sugar, the nucleobase, the phosphodiester linkage and/or the nucleotide phosphates. Such modifications include nucleotides comprising one or more ^{15}N, ^{13}C, ^{14}C, Deuterium, ^{3}H, ^{32}P, ^{125}I, ^{131}I atoms or other atoms or elements used as tracers.

In certain embodiments, an "end" modification incorporated into the guide RNA is selected from the group consisting of: PEG (polyethyleneglycol), hydrocarbon linkers (including: heteroatom (O,S,N)-substituted hydrocarbon spacers; halo-substituted hydrocarbon spacers; keto-, carboxyl-, amido-, thionyl-, carbamoyl-, thionocarbamaoyl-containing hydrocarbon spacers), spermine linkers, dyes including fluorescent dyes (for example fluoresceins, rhodamines, cyanines) attached to linkers such as for example 6-fluorescein-hexyl, quenchers (for example dabcyl, BHQ) and other labels (for example biotin, digoxigenin, acridine, streptavidin, avidin, peptides and/or proteins). In certain embodiments, an "end" modification comprises a conjugation (or ligation) of the guide RNA to another molecule comprising an oligonucleotide (comprising deoxynucleotides and/or ribonucleotides), a peptide, a protein, a sugar, an oligosaccharide, a steroid, a lipid, a folic acid, a vitamin and/or other molecule. In certain embodiments, an "end" modification incorporated into the guide RNA is located internally in the guide RNA sequence via a linker such as for example 2-(4-butylamidofluorescein)propane-1,3-diol bis (phosphodiester) linker (depicted below), which is incorporated as a phosphodiester linkage and can be incorporated anywhere between two nucleotides in the guide RNA.



2-(4-butylamidofluorescein)propane-1,3-diol bis(phosphodiester) linker

Other linkers include for example by way of illustration, but are not limited to:

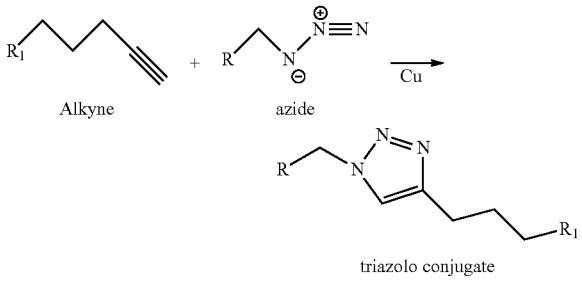


2-(3-(dye-amido)propanamido)propane-1,3-diol bis (phosphodiester) linker

In certain embodiments, the end modification comprises a terminal functional group such as an amine, a thiol (or sulfhydryl), a hydroxyl, a carboxyl, carbonyl, thionyl, thiocarbonyl, a carbamoyl, a thiocarbamoyl, a phoshoryl, an alkene, an alkyne, an halogen or a functional group-terminated linker, either of which can be subsequently conjugated to a desired moiety, for example a fluorescent dye or a non-fluorescent label or tag or any other molecule such as for example an oligonucleotide (comprising deoxynucleotides and/or ribonucleotides, including an aptamer), an amino acid, a peptide, a protein, a sugar, an oligosaccharide, a steroid, a lipid, a folic acid, a vitamin. The conjugation employs standard chemistry well-known in the art, including but not limited to coupling via N-hydroxysuccinimide, isothiocyanate, DCC (or DCI), and/or any other standart method as described in "Bioconjugate Techniques" by Greg T. Hermanson, Publisher Eslsevier Science, 3rd ed. (2013), the contents of which are incorporated herein by reference in their entireties.

In certain embodiments, the label or dye is attached or conjugated to a modified nucleotide in the gRNA. The conjugation of a fluorescent dye or other moiety such as a non-fluorescent label or tag (for example biotin, avidin, streptavidin, or moiety containing an isotopic label such as ^{15}N, ^{13}C, ^{14}C, Deuterium, ^{3}H, ^{32}P, ^{125}I and the like) or any other molecule such as for example an oligonucleotide (comprising deoxynucleotides and/or ribonucleotides

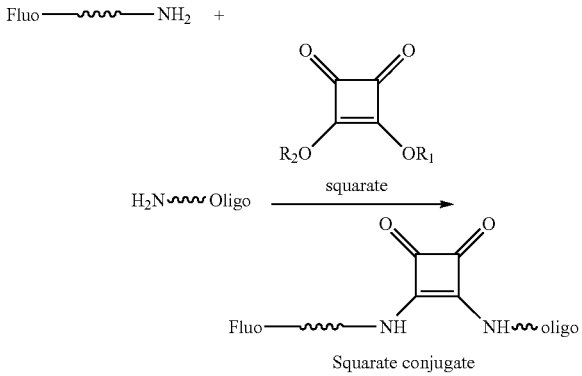
including an aptamer), an amino acid, a peptide, a protein, a sugar, an oligosaccharide, a steroid, a lipid, a folic acid, a vitamin or other molecule can be effectuated using the so-called "click" chemistry or the so-called "squarate" conjugation chemistry. The "click" chemistry refers to the [3+2] cycloaddition of an alkyne moiety with an azide moiety, leading to a triazolo linkage between the two moieties as shown in the following scheme:



as described for example in El-Sagheer, A. H. and Brown, T. "Click chemistry with DNA", *Chem. Soc. Rev.,* 2010, 39, 1388-1405 and Mojibul, H. M. and XiaoHua, P., DNA-associated click chemistry, *Sci. China Chem.,* 2014, 57:2, 215-31, the contents of which are hereby incorporated by reference in their entirety.

In certain embodiments, the conjugation can be effectuated by alternative cycloaddition such as Diels-Alder [4+2] cycloaddition of a π-conjugated diene moiety with an alkene moiety.

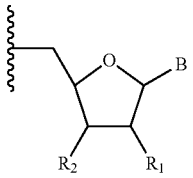
The "squarate" conjugation chemistry links two moieties each having an amine via a squarate derivative to result in a squarate conjugate that contains a squarate moiety (see e.g., Tietze et al. (1991) *Chem. Ber.,* 124, 1215-21, the contents of which are hereby incorporated by reference in their entirety). For example, a fluorescein containing a linker amine is conjugated to an oligoribonucleotide containing an amine through a squarate linker as described in the scheme below. An example of the squarate linker is depicted in the following scheme:



In certain embodiments, a chemical modification incorporated into the guide RNA is selected from the group consisting of 2'-O—C_{1-4}alkyl, 2'-H, 2'-O—C_{1-3}alkyl-O—C_{1-3}alkyl, 2'-F, 2'-NH_2, 2'-arabino, 2'-F-arabin, 4'-thioribosyl, 2-thioU, 2-thioC, 4-thioU, 6-thioG, 2-aminoA, 2-aminopurine, pseudouracil, hypoxanthine, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-methylC, 5-methylU, 5-hydroxymethylcytosine, 5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil, 5-allylU, 5-allylC, 5-aminoallyl-uracil, 5-aminoallyl-cytosine, an abasic nucleotide ("abN"), Z, P, UNA, isoC, isoG, 5-methyl-pyrimidine, x(A,G,C,T) and y(A,G,C,T), a phosphorothioate internucleotide linkage, a phosphonoacetate internucleotide linkage, a thiophosphonoacetate internucleotide linkage, a methylphosphonate internucleotide linkage, a boranophosphonate internucleotide linkage, a phosphorodithioate internucleotide linkage, 4'-thioribosyl nucleotide, a locked nucleic acid ("LNA") nucleotide, an unlocked nucleic acid ("ULNA") nucleotide, an alkyl spacer, a heteroalkyl (N, O, S) spacer, a 5'- and/or 3'-alkyl terminated nucleotide, a Unicap, a 5'-terminal cap known from nature, an xRNA base (analogous to "xDNA" base), an yRNA base (analogous to "yDNA" base), a PEG substituent, or a conjugated linker to a dye or non-fluorescent label (or tag) or other moiety as described above. Exemplary modified nucleotides are also depicted in Table 2.

TABLE 2

Exemplary modified nucleotides contained in a synthetic guide sequence.

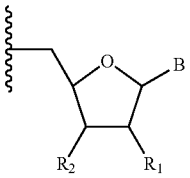


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
A1	OH	OH	uridine
A2	OMe	OH	uridine
A3	F	OH	uridine
A4	Cl	OH	uridine
A5	Br	OH	uridine
A6	I	OH	uridine
A7	NH_2	OH	uridine
A8	H	OH	uridine
A9	OH	phosphodiester	uridine
A10	OMe	phosphodiester	uridine
A11	F	phosphodiester	uridine
A12	Cl	phosphodiester	uridine
A13	Br	phosphodiester	uridine
A14	I	phosphodiester	uridine
A15	NH_2	phosphodiester	uridine
A16	H	phosphodiester	uridine
A17	OH	phosphonoacetate	uridine
A18	OMe	phosphonoacetate	uridine
A19	F	phosphonoacetate	uridine
A20	Cl	phosphonoacetate	uridine
A21	Br	phosphonoacetate	uridine
A22	I	phosphonoacetate	uridine
A23	NH_2	phosphonoacetate	uridine
A24	H	phosphonoacetate	uridine
A25	OH	thiophosphonoacetate	uridine
A26	OMe	thiophosphonoacetate	uridine
A27	F	thiophosphonoacetate	uridine
A28	Cl	thiophosphonoacetate	uridine
A29	Br	thiophosphonoacetate	uridine
A30	I	thiophosphonoacetate	uridine
A31	NH_2	thiophosphonoacetate	uridine
A32	H	thiophosphonoacetate	uridine
A33	OH	phosphorothioate	uridine
A34	OMe	phosphorothioate	uridine
A35	F	phosphorothioate	uridine
A36	Cl	phosphorothioate	uridine
A37	Br	phosphorothioate	uridine
A38	I	phosphorothioate	uridine
A39	NH_2	phosphorothioate	uridine
A40	H	phosphorothioate	uridine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

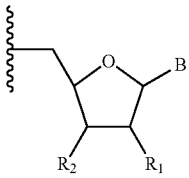


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
A41	OH	phosphorodithioate	uridine
A42	OMe	phosphorodithioate	uridine
A43	F	phosphorodithioate	uridine
A44	Cl	phosphorodithioate	uridine
A45	Br	phosphorodithioate	uridine
A46	I	phosphorodithioate	uridine
A47	NH_2	phosphorodithioate	uridine
A48	H	phosphorodithioate	uridine
A49	OH	methylphosphonate	uridine
A50	OMe	methylphosphonate	uridine
A51	F	methylphosphonate	uridine
A52	Cl	methylphosphonate	uridine
A53	Br	methylphosphonate	uridine
A54	I	methylphosphonate	uridine
A55	NH_2	methylphosphonate	uridine
A56	H	methylphosphonate	uridine
A57	OH	boranophosphonate	uridine
A58	OMe	boranophosphonate	uridine
A59	F	boranophosphonate	uridine
A60	Cl	boranophosphonate	uridine
A61	Br	boranophosphonate	uridine
A62	I	boranophosphonate	uridine
A63	NH_2	boranophosphonate	uridine
A64	H	boranophosphonate	uridine
B1	OH	OH	adenosine
B2	OMe	OH	adenosine
B3	F	OH	adenosine
B4	Cl	OH	adenosine
B5	Br	OH	adenosine
B6	I	OH	adenosine
B7	NH_2	OH	adenosine
B8	H	OH	adenosine
B9	OH	phosphodiester	adenosine
B10	OMe	phosphodiester	adenosine
B11	F	phosphodiester	adenosine
B12	Cl	phosphodiester	adenosine
B13	Br	phosphodiester	adenosine
B14	I	phosphodiester	adenosine
B15	NH_2	phosphodiester	adenosine
B16	H	phosphodiester	adenosine
B17	OH	phosphonoacetate	adenosine
B18	OMe	phosphonoacetate	adenosine
B19	F	phosphonoacetate	adenosine
B20	Cl	phosphonoacetate	adenosine
B21	Br	phosphonoacetate	adenosine
B22	I	phosphonoacetate	adenosine
B23	NH_2	phosphonoacetate	adenosine
B24	H	phosphonoacetate	adenosine
B25	OH	thiophosphonoacetate	adenosine
B26	OMe	thiophosphonoacetate	adenosine
B27	F	thiophosphonoacetate	adenosine
B28	Cl	thiophosphonoacetate	adenosine
B29	Br	thiophosphonoacetate	adenosine
B30	I	thiophosphonoacetate	adenosine
B31	NH_2	thiophosphonoacetate	adenosine
B32	H	thiophosphonoacetate	adenosine
B33	OH	phosphorothioate	adenosine
B34	OMe	phosphorothioate	adenosine
B35	F	phosphorothioate	adenosine
B36	Cl	phosphorothioate	adenosine
B37	Br	phosphorothioate	adenosine
B38	I	phosphorothioate	adenosine
B39	NH_2	phosphorothioate	adenosine
B40	H	phosphorothioate	adenosine
B41	OH	phosphorodithioate	adenosine
B42	OMe	phosphorodithioate	adenosine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

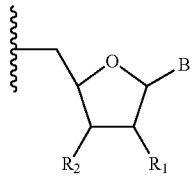


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
B43	F	phosphorodithioate	adenosine
B44	Cl	phosphorodithioate	adenosine
B45	Br	phosphorodithioate	adenosine
B46	I	phosphorodithioate	adenosine
B47	NH_2	phosphorodithioate	adenosine
B48	H	phosphorodithioate	adenosine
B49	OH	methylphosphonate	adenosine
B50	OMe	methylphosphonate	adenosine
B51	F	methylphosphonate	adenosine
B52	Cl	methylphosphonate	adenosine
B53	Br	methylphosphonate	adenosine
B54	I	methylphosphonate	adenosine
B55	NH_2	methylphosphonate	adenosine
B56	H	methylphosphonate	adenosine
B57	OH	boranophosphonate	adenosine
B58	OMe	boranophosphonate	adenosine
B59	F	boranophosphonate	adenosine
B60	Cl	boranophosphonate	adenosine
B61	Br	boranophosphonate	adenosine
B62	I	boranophosphonate	adenosine
B63	NH_2	boranophosphonate	adenosine
B64	H	boranophosphonate	adenosine
C1	OH	OH	cytidine
C2	OMe	OH	cytidine
C3	F	OH	cytidine
C4	Cl	OH	cytidine
C5	Br	OH	cytidine
C6	I	OH	cytidine
C7	NH_2	OH	cytidine
C8	H	OH	cytidine
C9	OH	phosphodiester	cytidine
C10	OMe	phosphodiester	cytidine
C11	F	phosphodiester	cytidine
C12	Cl	phosphodiester	cytidine
C13	Br	phosphodiester	cytidine
C14	I	phosphodiester	cytidine
C15	NH_2	phosphodiester	cytidine
C16	H	phosphodiester	cytidine
C17	OH	phosphonoacetate	cytidine
C18	OMe	phosphonoacetate	cytidine
C19	F	phosphonoacetate	cytidine
C20	Cl	phosphonoacetate	cytidine
C21	Br	phosphonoacetate	cytidine
C22	I	phosphonoacetate	cytidine
C23	NH_2	phosphonoacetate	cytidine
C24	H	phosphonoacetate	cytidine
C25	OH	thiophosphonoacetate	cytidine
C26	OMe	thiophosphonoacetate	cytidine
C27	F	thiophosphonoacetate	cytidine
C28	Cl	thiophosphonoacetate	cytidine
C29	Br	thiophosphonoacetate	cytidine
C30	I	thiophosphonoacetate	cytidine
C31	NH_2	thiophosphonoacetate	cytidine
C32	H	thiophosphonoacetate	cytidine
C33	OH	phosphorothioate	cytidine
C34	OMe	phosphorothioate	cytidine
C35	F	phosphorothioate	cytidine
C36	Cl	phosphorothioate	cytidine
C37	Br	phosphorothioate	cytidine
C38	I	phosphorothioate	cytidine
C39	NH_2	phosphorothioate	cytidine
C40	H	phosphorothioate	cytidine
C41	OH	phosphorodithioate	cytidine
C42	OMe	phosphorodithioate	cytidine
C43	F	phosphorodithioate	cytidine
C44	Cl	phosphorodithioate	cytidine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

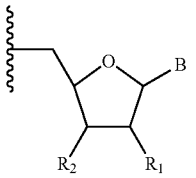


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
C45	Br	phosphorodithioate	cytidine
C46	I	phosphorodithioate	cytidine
C47	NH_2	phosphorodithioate	cytidine
C48	H	phosphorodithioate	cytidine
C49	OH	methylphosphonate	cytidine
C50	OMe	methylphosphonate	cytidine
C51	F	methylphosphonate	cytidine
C52	Cl	methylphosphonate	cytidine
C53	Br	methylphosphonate	cytidine
C54	I	methylphosphonate	cytidine
C55	NH_2	methylphosphonate	cytidine
C56	H	methylphosphonate	cytidine
C57	OH	boranophosphonate	cytidine
C58	OMe	boranophosphonate	cytidine
C59	F	boranophosphonate	cytidine
C60	Cl	boranophosphonate	cytidine
C61	Br	boranophosphonate	cytidine
C62	I	boranophosphonate	cytidine
C63	NH_2	boranophosphonate	cytidine
C64	H	boranophosphonate	cytidine
D1	OH	OH	guanosine
D2	OMe	OH	guanosine
D3	F	OH	guanosine
D4	Cl	OH	guanosine
D5	Br	OH	guanosine
D6	I	OH	guanosine
D7	NH_2	OH	guanosine
D8	H	OH	guanosine
D9	OH	phosphodiester	guanosine
D10	OMe	phosphodiester	guanosine
D11	F	phosphodiester	guanosine
D12	Cl	phosphodiester	guanosine
D13	Br	phosphodiester	guanosine
D14	I	phosphodiester	guanosine
D15	NH_2	phosphodiester	guanosine
D16	H	phosphodiester	guanosine
D17	OH	phosphonoacetate	guanosine
D18	OMe	phosphonoacetate	guanosine
D19	F	phosphonoacetate	guanosine
D20	Cl	phosphonoacetate	guanosine
D21	Br	phosphonoacetate	guanosine
D22	I	phosphonoacetate	guanosine
D23	NH_2	phosphonoacetate	guanosine
D24	H	phosphonoacetate	guanosine
D25	OH	thiophosphonoacetate	guanosine
D26	OMe	thiophosphonoacetate	guanosine
D27	F	thiophosphonoacetate	guanosine
D28	Cl	thiophosphonoacetate	guanosine
D29	Br	thiophosphonoacetate	guanosine
D30	I	thiophosphonoacetate	guanosine
D31	NH_2	thiophosphonoacetate	guanosine
D32	H	thiophosphonoacetate	guanosine
D33	OH	phosphorothioate	guanosine
D34	OMe	phosphorothioate	guanosine
D35	F	phosphorothioate	guanosine
D36	Cl	phosphorothioate	guanosine
D37	Br	phosphorothioate	guanosine
D38	I	phosphorothioate	guanosine
D39	NH_2	phosphorothioate	guanosine
D40	H	phosphorothioate	guanosine
D41	OH	phosphorodithioate	guanosine
D42	OMe	phosphorodithioate	guanosine
D43	F	phosphorodithioate	guanosine
D44	Cl	phosphorodithioate	guanosine
D45	Br	phosphorodithioate	guanosine
D46	I	phosphorodithioate	guanosine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

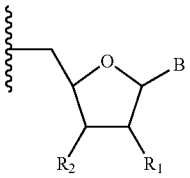


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
D47	NH_2	phosphorodithioate	guanosine
D48	H	phosphorodithioate	guanosine
D49	OH	methylphosphonate	guanosine
D50	OMe	methylphosphonate	guanosine
D51	F	methylphosphonate	guanosine
D52	Cl	methylphosphonate	guanosine
D53	Br	methylphosphonate	guanosine
D54	I	methylphosphonate	guanosine
D55	NH_2	methylphosphonate	guanosine
D56	H	methylphosphonate	guanosine
D57	OH	boranophosphonate	guanosine
D58	OMe	boranophosphonate	guanosine
D59	F	boranophosphonate	guanosine
D60	Cl	boranophosphonate	guanosine
D61	Br	boranophosphonate	guanosine
D62	I	boranophosphonate	guanosine
D63	NH_2	boranophosphonate	guanosine
D64	H	boranophosphonate	guanosine
E1	OH	OH	2-thiouridine
E2	OMe	OH	2-thiouridine
E3	F	OH	2-thiouridine
E4	Cl	OH	2-thiouridine
E5	Br	OH	2-thiouridine
E6	I	OH	2-thiouridine
E7	NH_2	OH	2-thiouridine
E8	H	OH	2-thiouridine
E9	OH	phosphodiester	2-thiouridine
E10	OMe	phosphodiester	2-thiouridine
E11	F	phosphodiester	2-thiouridine
E12	Cl	phosphodiester	2-thiouridine
E13	Br	phosphodiester	2-thiouridine
E14	I	phosphodiester	2-thiouridine
E15	NH_2	phosphodiester	2-thiouridine
E16	H	phosphodiester	2-thiouridine
E17	OH	phosphonoacetate	2-thiouridine
E18	OMe	phosphonoacetate	2-thiouridine
E19	F	phosphonoacetate	2-thiouridine
E20	Cl	phosphonoacetate	2-thiouridine
E21	Br	phosphonoacetate	2-thiouridine
E22	I	phosphonoacetate	2-thiouridine
E23	NH_2	phosphonoacetate	2-thiouridine
E24	H	phosphonoacetate	2-thiouridine
E25	OH	thiophosphonoacetate	2-thiouridine
E26	OMe	thiophosphonoacetate	2-thiouridine
E27	F	thiophosphonoacetate	2-thiouridine
E28	Cl	thiophosphonoacetate	2-thiouridine
E29	Br	thiophosphonoacetate	2-thiouridine
E30	I	thiophosphonoacetate	2-thiouridine
E31	NH_2	thiophosphonoacetate	2-thiouridine
E32	H	thiophosphonoacetate	2-thiouridine
E33	OH	phosphorothioate	2-thiouridine
E34	OMe	phosphorothioate	2-thiouridine
E35	F	phosphorothioate	2-thiouridine
E36	Cl	phosphorothioate	2-thiouridine
E37	Br	phosphorothioate	2-thiouridine
E38	I	phosphorothioate	2-thiouridine
E39	NH_2	phosphorothioate	2-thiouridine
E40	H	phosphorothioate	2-thiouridine
E41	OH	phosphorodithioate	2-thiouridine
E42	OMe	phosphorodithioate	2-thiouridine
E43	F	phosphorodithioate	2-thiouridine
E44	Cl	phosphorodithioate	2-thiouridine
E45	Br	phosphorodithioate	2-thiouridine
E46	I	phosphorodithioate	2-thiouridine
E47	NH_2	phosphorodithioate	2-thiouridine
E48	H	phosphorodithioate	2-thiouridine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

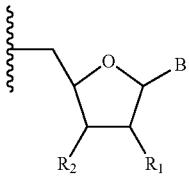


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
E49	OH	methylphosphonate	2-thiouridine
E50	OMe	methylphosphonate	2-thiouridine
E51	F	methylphosphonate	2-thiouridine
E52	Cl	methylphosphonate	2-thiouridine
E53	Br	methylphosphonate	2-thiouridine
E54	I	methylphosphonate	2-thiouridine
E55	NH_2	methylphosphonate	2-thiouridine
E56	H	methylphosphonate	2-thiouridine
E57	OH	boranophosphonate	2-thiouridine
E58	OMe	boranophosphonate	2-thiouridine
E59	F	boranophosphonate	2-thiouridine
E60	Cl	boranophosphonate	2-thiouridine
E61	Br	boranophosphonate	2-thiouridine
E62	I	boranophosphonate	2-thiouridine
E63	NH_2	boranophosphonate	2-thiouridine
E64	H	boranophosphonate	2-thiouridine
F1	OH	OH	4-thiouridine
F2	OMe	OH	4-thiouridine
F3	F	OH	4-thiouridine
F4	Cl	OH	4-thiouridine
F5	Br	OH	4-thiouridine
F6	I	OH	4-thiouridine
F7	NH_2	OH	4-thiouridine
F8	H	OH	4-thiouridine
F9	OH	phosphodiester	4-thiouridine
F10	OMe	phosphodiester	4-thiouridine
F11	F	phosphodiester	4-thiouridine
F12	Cl	phosphodiester	4-thiouridine
F13	Br	phosphodiester	4-thiouridine
F14	I	phosphodiester	4-thiouridine
F15	NH_2	phosphodiester	4-thiouridine
F16	H	phosphodiester	4-thiouridine
F17	OH	phosphonoacetate	4-thiouridine
F18	OMe	phosphonoacetate	4-thiouridine
F19	F	phosphonoacetate	4-thiouridine
F20	Cl	phosphonoacetate	4-thiouridine
F21	Br	phosphonoacetate	4-thiouridine
F22	I	phosphonoacetate	4-thiouridine
F23	NH_2	phosphonoacetate	4-thiouridine
F24	H	phosphonoacetate	4-thiouridine
F25	OH	thiophosphonoacetate	4-thiouridine
F26	OMe	thiophosphonoacetate	4-thiouridine
F27	F	thiophosphonoacetate	4-thiouridine
F28	Cl	thiophosphonoacetate	4-thiouridine
F29	Br	thiophosphonoacetate	4-thiouridine
F30	I	thiophosphonoacetate	4-thiouridine
F31	NH_2	thiophosphonoacetate	4-thiouridine
F32	H	thiophosphonoacetate	4-thiouridine
F33	OH	phosphorothioate	4-thiouridine
F34	OMe	phosphorothioate	4-thiouridine
F35	F	phosphorothioate	4-thiouridine
F36	Cl	phosphorothioate	4-thiouridine
F37	Br	phosphorothioate	4-thiouridine
F38	I	phosphorothioate	4-thiouridine
F39	NH_2	phosphorothioate	4-thiouridine
F40	H	phosphorothioate	4-thiouridine
F41	OH	phosphorodithioate	4-thiouridine
F42	OMe	phosphorodithioate	4-thiouridine
F43	F	phosphorodithioate	4-thiouridine
F44	Cl	phosphorodithioate	4-thiouridine
F45	Br	phosphorodithioate	4-thiouridine
F46	I	phosphorodithioate	4-thiouridine
F47	NH_2	phosphorodithioate	4-thiouridine
F48	H	phosphorodithioate	4-thiouridine
F49	OH	methylphosphonate	4-thiouridine
F50	OMe	methylphosphonate	4-thiouridine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

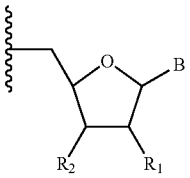


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
F51	F	methylphosphonate	4-thiouridine
F52	Cl	methylphosphonate	4-thiouridine
F53	Br	methylphosphonate	4-thiouridine
F54	I	methylphosphonate	4-thiouridine
F55	NH_2	methylphosphonate	4-thiouridine
F56	H	methylphosphonate	4-thiouridine
F57	OH	boranophosphonate	4-thiouridine
F58	OMe	boranophosphonate	4-thiouridine
F59	F	boranophosphonate	4-thiouridine
F60	Cl	boranophosphonate	4-thiouridine
F61	Br	boranophosphonate	4-thiouridine
F62	I	boranophosphonate	4-thiouridine
F63	NH_2	boranophosphonate	4-thiouridine
F64	H	boranophosphonate	4-thiouridine
G1	OH	OH	2-aminoadenosine
G2	OMe	OH	2-aminoadenosine
G3	F	OH	2-aminoadenosine
G4	Cl	OH	2-aminoadenosine
G5	Br	OH	2-aminoadenosine
G6	I	OH	2-aminoadenosine
G7	NH_2	OH	2-aminoadenosine
G8	H	OH	2-aminoadenosine
G9	OH	phosphodiester	2-aminoadenosine
G10	OMe	phosphodiester	2-aminoadenosine
G11	F	phosphodiester	2-aminoadenosine
G12	Cl	phosphodiester	2-aminoadenosine
G13	Br	phosphodiester	2-aminoadenosine
G14	I	phosphodiester	2-aminoadenosine
G15	NH_2	phosphodiester	2-aminoadenosine
G16	H	phosphodiester	2-aminoadenosine
G17	OH	phosphonoacetate	2-aminoadenosine
G18	OMe	phosphonoacetate	2-aminoadenosine
G19	F	phosphonoacetate	2-aminoadenosine
G20	Cl	phosphonoacetate	2-aminoadenosine
G21	Br	phosphonoacetate	2-aminoadenosine
G22	I	phosphonoacetate	2-aminoadenosine
G23	NH_2	phosphonoacetate	2-aminoadenosine
G24	H	phosphonoacetate	2-aminoadenosine
G25	OH	thiophosphonoacetate	2-aminoadenosine
G26	OMe	thiophosphonoacetate	2-aminoadenosine
G27	F	thiophosphonoacetate	2-aminoadenosine
G28	Cl	thiophosphonoacetate	2-aminoadenosine
G29	Br	thiophosphonoacetate	2-aminoadenosine
G30	I	thiophosphonoacetate	2-aminoadenosine
G31	NH_2	thiophosphonoacetate	2-aminoadenosine
G32	H	thiophosphonoacetate	2-aminoadenosine
G33	OH	phosphorothioate	2-aminoadenosine
G34	OMe	phosphorothioate	2-aminoadenosine
G35	F	phosphorothioate	2-aminoadenosine
G36	Cl	phosphorothioate	2-aminoadenosine
G37	Br	phosphorothioate	2-aminoadenosine
G38	I	phosphorothioate	2-aminoadenosine
G39	NH_2	phosphorothioate	2-aminoadenosine
G40	H	phosphorothioate	2-aminoadenosine
G41	OH	phosphorodithioate	2-aminoadenosine
G42	OMe	phosphorodithioate	2-aminoadenosine
G43	F	phosphorodithioate	2-aminoadenosine
G44	Cl	phosphorodithioate	2-aminoadenosine
G45	Br	phosphorodithioate	2-aminoadenosine
G46	I	phosphorodithioate	2-aminoadenosine
G47	NH_2	phosphorodithioate	2-aminoadenosine
G48	H	phosphorodithioate	2-aminoadenosine
G49	OH	methylphosphonate	2-aminoadenosine
G50	OMe	methylphosphonate	2-aminoadenosine
G51	F	methylphosphonate	2-aminoadenosine
G52	Cl	methylphosphonate	2-aminoadenosine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

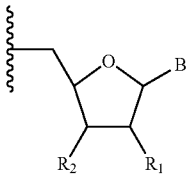


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
G53	Br	methylphosphonate	2-aminoadenosine
G54	I	methylphosphonate	2-aminoadenosine
G55	NH_2	methylphosphonate	2-aminoadenosine
G56	H	methylphosphonate	2-aminoadenosine
G57	OH	boranophosphonate	2-aminoadenosine
G58	OMe	boranophosphonate	2-aminoadenosine
G59	F	boranophosphonate	2-aminoadenosine
G60	Cl	boranophosphonate	2-aminoadenosine
G61	Br	boranophosphonate	2-aminoadenosine
G62	I	boranophosphonate	2-aminoadenosine
G63	NH_2	boranophosphonate	2-aminoadenosine
G64	H	boranophosphonate	2-aminoadenosine
H1	OH	OH	7-deazaguanosine
H2	OMe	OH	7-deazaguanosine
H3	F	OH	7-deazaguanosine
H4	Cl	OH	7-deazaguanosine
H5	Br	OH	7-deazaguanosine
H6	I	OH	7-deazaguanosine
H7	NH_2	OH	7-deazaguanosine
H8	H	OH	7-deazaguanosine
H9	OH	phosphodiester	7-deazaguanosine
H10	OMe	phosphodiester	7-deazaguanosine
H11	F	phosphodiester	7-deazaguanosine
H12	Cl	phosphodiester	7-deazaguanosine
H13	Br	phosphodiester	7-deazaguanosine
H14	I	phosphodiester	7-deazaguanosine
H15	NH_2	phosphodiester	7-deazaguanosine
H16	H	phosphodiester	7-deazaguanosine
H17	OH	phosphonoacetate	7-deazaguanosine
H18	OMe	phosphonoacetate	7-deazaguanosine
H19	F	phosphonoacetate	7-deazaguanosine
H20	Cl	phosphonoacetate	7-deazaguanosine
H21	Br	phosphonoacetate	7-deazaguanosine
H22	I	phosphonoacetate	7-deazaguanosine
H23	NH_2	phosphonoacetate	7-deazaguanosine
H24	H	phosphonoacetate	7-deazaguanosine
H25	OH	thiophosphonoacetate	7-deazaguanosine
H26	OMe	thiophosphonoacetate	7-deazaguanosine
H27	F	thiophosphonoacetate	7-deazaguanosine
H28	Cl	thiophosphonoacetate	7-deazaguanosine
H29	Br	thiophosphonoacetate	7-deazaguanosine
H30	I	thiophosphonoacetate	7-deazaguanosine
H31	NH_2	thiophosphonoacetate	7-deazaguanosine
H32	H	thiophosphonoacetate	7-deazaguanosine
H33	OH	phosphorothioate	7-deazaguanosine
H34	OMe	phosphorothioate	7-deazaguanosine
H35	F	phosphorothioate	7-deazaguanosine
H36	Cl	phosphorothioate	7-deazaguanosine
H37	Br	phosphorothioate	7-deazaguanosine
H38	I	phosphorothioate	7-deazaguanosine
H39	NH_2	phosphorothioate	7-deazaguanosine
H40	H	phosphorothioate	7-deazaguanosine
H41	OH	phosphorodithioate	7-deazaguanosine
H42	OMe	phosphorodithioate	7-deazaguanosine
H43	F	phosphorodithioate	7-deazaguanosine
H44	Cl	phosphorodithioate	7-deazaguanosine
H45	Br	phosphorodithioate	7-deazaguanosine
H46	I	phosphorodithioate	7-deazaguanosine
H47	NH_2	phosphorodithioate	7-deazaguanosine
H48	H	phosphorodithioate	7-deazaguanosine
H49	OH	methylphosphonate	7-deazaguanosine
H50	OMe	methylphosphonate	7-deazaguanosine
H51	F	methylphosphonate	7-deazaguanosine
H52	Cl	methylphosphonate	7-deazaguanosine
H53	Br	methylphosphonate	7-deazaguanosine
H54	I	methylphosphonate	7-deazaguanosine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

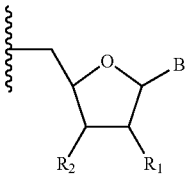


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
H55	NH_2	methylphosphonate	7-deazaguanosine
H56	H	methylphosphonate	7-deazaguanosine
H57	OH	boranophosphonate	7-deazaguanosine
H58	OMe	boranophosphonate	7-deazaguanosine
H59	F	boranophosphonate	7-deazaguanosine
H60	Cl	boranophosphonate	7-deazaguanosine
H61	Br	boranophosphonate	7-deazaguanosine
H62	I	boranophosphonate	7-deazaguanosine
H63	NH_2	boranophosphonate	7-deazaguanosine
H64	H	boranophosphonate	7-deazaguanosine
I1	OH	OH	inosine
I2	OMe	OH	inosine
I3	F	OH	inosine
I4	Cl	OH	inosine
I5	Br	OH	inosine
I6	I	OH	inosine
I7	NH_2	OH	inosine
I8	H	OH	inosine
I9	OH	phosphodiester	inosine
I10	OMe	phosphodiester	inosine
I11	F	phosphodiester	inosine
I12	Cl	phosphodiester	inosine
I13	Br	phosphodiester	inosine
I14	I	phosphodiester	inosine
I15	NH_2	phosphodiester	inosine
I16	H	phosphodiester	inosine
I17	OH	phosphonoacetate	inosine
I18	OMe	phosphonoacetate	inosine
I19	F	phosphonoacetate	inosine
I20	Cl	phosphonoacetate	inosine
I21	Br	phosphonoacetate	inosine
I22	I	phosphonoacetate	inosine
I23	NH_2	phosphonoacetate	inosine
I24	H	phosphonoacetate	inosine
I25	OH	thiophosphonoacetate	inosine
I26	OMe	thiophosphonoacetate	inosine
I27	F	thiophosphonoacetate	inosine
I28	Cl	thiophosphonoacetate	inosine
I29	Br	thiophosphonoacetate	inosine
I30	I	thiophosphonoacetate	inosine
I31	NH_2	thiophosphonoacetate	inosine
I32	H	thiophosphonoacetate	inosine
I33	OH	phosphorothioate	inosine
I34	OMe	phosphorothioate	inosine
I35	F	phosphorothioate	inosine
I36	Cl	phosphorothioate	inosine
I37	Br	phosphorothioate	inosine
I38	I	phosphorothioate	inosine
I39	NH_2	phosphorothioate	inosine
I40	H	phosphorothioate	inosine
I41	OH	phosphorodithioate	inosine
I42	OMe	phosphorodithioate	inosine
I43	F	phosphorodithioate	inosine
I44	Cl	phosphorodithioate	inosine
I45	Br	phosphorodithioate	inosine
I46	I	phosphorodithioate	inosine
I47	NH_2	phosphorodithioate	inosine
I48	H	phosphorodithioate	inosine
I49	OH	methylphosphonate	inosine
I50	OMe	methylphosphonate	inosine
I51	F	methylphosphonate	inosine
I52	Cl	methylphosphonate	inosine
I53	Br	methylphosphonate	inosine
I54	I	methylphosphonate	inosine
I55	NH_2	methylphosphonate	inosine
I56	H	methylphosphonate	inosine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

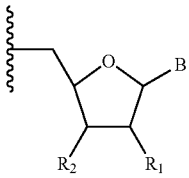


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
I57	OH	boranophosphonate	inosine
I58	OMe	boranophosphonate	inosine
I59	F	boranophosphonate	inosine
I60	Cl	boranophosphonate	inosine
I61	Br	boranophosphonate	inosine
I62	I	boranophosphonate	inosine
I63	NH_2	boranophosphonate	inosine
I64	H	boranophosphonate	inosine
J1	OH	OH	5-methylcytidine
J2	OMe	OH	5-methylcytidine
J3	F	OH	5-methylcytidine
J4	Cl	OH	5-methylcytidine
J5	Br	OH	5-methylcytidine
J6	I	OH	5-methylcytidine
J7	NH_2	OH	5-methylcytidine
J8	H	OH	5-methylcytidine
J9	OH	phosphodiester	5-methylcytidine
J10	OMe	phosphodiester	5-methylcytidine
J11	F	phosphodiester	5-methylcytidine
J12	Cl	phosphodiester	5-methylcytidine
J13	Br	phosphodiester	5-methylcytidine
J14	I	phosphodiester	5-methylcytidine
J15	NH_2	phosphodiester	5-methylcytidine
J16	H	phosphodiester	5-methylcytidine
J17	OH	phosphonoacetate	5-methylcytidine
J18	OMe	phosphonoacetate	5-methylcytidine
J19	F	phosphonoacetate	5-methylcytidine
J20	Cl	phosphonoacetate	5-methylcytidine
J21	Br	phosphonoacetate	5-methylcytidine
J22	I	phosphonoacetate	5-methylcytidine
J23	NH_2	phosphonoacetate	5-methylcytidine
J24	H	phosphonoacetate	5-methylcytidine
J25	OH	thiophosphonoacetate	5-methylcytidine
J26	OMe	thiophosphonoacetate	5-methylcytidine
J27	F	thiophosphonoacetate	5-methylcytidine
J28	Cl	thiophosphonoacetate	5-methylcytidine
J29	Br	thiophosphonoacetate	5-methylcytidine
J30	I	thiophosphonoacetate	5-methylcytidine
J31	NH_2	thiophosphonoacetate	5-methylcytidine
J32	H	thiophosphonoacetate	5-methylcytidine
J33	OH	phosphorothioate	5-methylcytidine
J34	OMe	phosphorothioate	5-methylcytidine
J35	F	phosphorothioate	5-methylcytidine
J36	Cl	phosphorothioate	5-methylcytidine
J37	Br	phosphorothioate	5-methylcytidine
J38	I	phosphorothioate	5-methylcytidine
J39	NH_2	phosphorothioate	5-methylcytidine
J40	H	phosphorothioate	5-methylcytidine
J41	OH	phosphorodithioate	5-methylcytidine
J42	OMe	phosphorodithioate	5-methylcytidine
J43	F	phosphorodithioate	5-methylcytidine
J44	Cl	phosphorodithioate	5-methylcytidine
J45	Br	phosphorodithioate	5-methylcytidine
J46	I	phosphorodithioate	5-methylcytidine
J47	NH_2	phosphorodithioate	5-methylcytidine
J48	H	phosphorodithioate	5-methylcytidine
J49	OH	methylphosphonate	5-methylcytidine
J50	OMe	methylphosphonate	5-methylcytidine
J51	F	methylphosphonate	5-methylcytidine
J52	Cl	methylphosphonate	5-methylcytidine
J53	Br	methylphosphonate	5-methylcytidine
J54	I	methylphosphonate	5-methylcytidine
J55	NH_2	methylphosphonate	5-methylcytidine
J56	H	methylphosphonate	5-methylcytidine
J57	OH	boranophosphonate	5-methylcytidine
J58	OMe	boranophosphonate	5-methylcytidine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

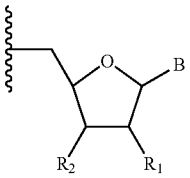


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
J59	F	boranophosphonate	5-methylcytidine
J60	Cl	boranophosphonate	5-methylcytidine
J61	Br	boranophosphonate	5-methylcytidine
J62	I	boranophosphonate	5-methylcytidine
J63	NH_2	boranophosphonate	5-methylcytidine
J64	H	boranophosphonate	5-methylcytidine
K1	OH	OH	5-aminoallyluridine
K2	OMe	OH	5-aminoallyluridine
K3	F	OH	5-aminoallyluridine
K4	Cl	OH	5-aminoallyluridine
K5	Br	OH	5-aminoallyluridine
K6	I	OH	5-aminoallyluridine
K7	NH_2	OH	5-aminoallyluridine
K8	H	OH	5-aminoallyluridine
K9	OH	phosphodiester	5-aminoallyluridine
K10	OMe	phosphodiester	5-aminoallyluridine
K11	F	phosphodiester	5-aminoallyluridine
K12	Cl	phosphodiester	5-aminoallyluridine
K13	Br	phosphodiester	5-aminoallyluridine
K14	I	phosphodiester	5-aminoallyluridine
K15	NH_2	phosphodiester	5-aminoallyluridine
K16	H	phosphodiester	5-aminoallyluridine
K17	OH	phosphonoacetate	5-aminoallyluridine
K18	OMe	phosphonoacetate	5-aminoallyluridine
K19	F	phosphonoacetate	5-aminoallyluridine
K20	Cl	phosphonoacetate	5-aminoallyluridine
K21	Br	phosphonoacetate	5-aminoallyluridine
K22	I	phosphonoacetate	5-aminoallyluridine
K23	NH_2	phosphonoacetate	5-aminoallyluridine
K24	H	phosphonoacetate	5-aminoallyluridine
K25	OH	thiophosphonoacetate	5-aminoallyluridine
K26	OMe	thiophosphonoacetate	5-aminoallyluridine
K27	F	thiophosphonoacetate	5-aminoallyluridine
K28	Cl	thiophosphonoacetate	5-aminoallyluridine
K29	Br	thiophosphonoacetate	5-aminoallyluridine
K30	I	thiophosphonoacetate	5-aminoallyluridine
K31	NH_2	thiophosphonoacetate	5-aminoallyluridine
K32	H	thiophosphonoacetate	5-aminoallyluridine
K33	OH	phosphorothioate	5-aminoallyluridine
K34	OMe	phosphorothioate	5-aminoallyluridine
K35	F	phosphorothioate	5-aminoallyluridine
K36	Cl	phosphorothioate	5-aminoallyluridine
K37	Br	phosphorothioate	5-aminoallyluridine
K38	I	phosphorothioate	5-aminoallyluridine
K39	NH_2	phosphorothioate	5-aminoallyluridine
K40	H	phosphorothioate	5-aminoallyluridine
K41	OH	phosphorodithioate	5-aminoallyluridine
K42	OMe	phosphorodithioate	5-aminoallyluridine
K43	F	phosphorodithioate	5-aminoallyluridine
K44	Cl	phosphorodithioate	5-aminoallyluridine
K45	Br	phosphorodithioate	5-aminoallyluridine
K46	I	phosphorodithioate	5-aminoallyluridine
K47	NH_2	phosphorodithioate	5-aminoallyluridine
K48	H	phosphorodithioate	5-aminoallyluridine
K49	OH	methylphosphonate	5-aminoallyluridine
K50	OMe	methylphosphonate	5-aminoallyluridine
K51	F	methylphosphonate	5-aminoallyluridine
K52	Cl	methylphosphonate	5-aminoallyluridine
K53	Br	methylphosphonate	5-aminoallyluridine
K54	I	methylphosphonate	5-aminoallyluridine
K55	NH_2	methylphosphonate	5-aminoallyluridine
K56	H	methylphosphonate	5-aminoallyluridine
K57	OH	boranophosphonate	5-aminoallyluridine
K58	OMe	boranophosphonate	5-aminoallyluridine
K59	F	boranophosphonate	5-aminoallyluridine
K60	Cl	boranophosphonate	5-aminoallyluridine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.

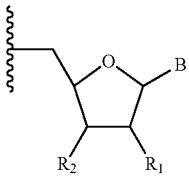


R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
K61	Br	boranophosphonate	5-aminoallyluridine
K62	I	boranophosphonate	5-aminoallyluridine
K63	NH_2	boranophosphonate	5-aminoallyluridine
K64	H	boranophosphonate	5-aminoallyluridine
L1	OH	OH	5-methyluridine
L2	OMe	OH	5-methyluridine
L3	F	OH	5-methyluridine
L4	Cl	OH	5-methyluridine
L5	Br	OH	5-methyluridine
L6	I	OH	5-methyluridine
L7	NH_2	OH	5-methyluridine
L8	H	OH	5-methyluridine
L9	OH	phosphodiester	5-methyluridine
L10	OMe	phosphodiester	5-methyluridine
L11	F	phosphodiester	5-methyluridine
L12	Cl	phosphodiester	5-methyluridine
L13	Br	phosphodiester	5-methyluridine
L14	I	phosphodiester	5-methyluridine
L15	NH_2	phosphodiester	5-methyluridine
L16	H	phosphodiester	5-methyluridine
L17	OH	phosphonoacetate	5-methyluridine
L18	OMe	phosphonoacetate	5-methyluridine
L19	F	phosphonoacetate	5-methyluridine
L20	Cl	phosphonoacetate	5-methyluridine
L21	Br	phosphonoacetate	5-methyluridine
L22	I	phosphonoacetate	5-methyluridine
L23	NH_2	phosphonoacetate	5-methyluridine
L24	H	phosphonoacetate	5-methyluridine
L25	OH	thiophosphonoacetate	5-methyluridine
L26	OMe	thiophosphonoacetate	5-methyluridine
L27	F	thiophosphonoacetate	5-methyluridine
L28	Cl	thiophosphonoacetate	5-methyluridine
L29	Br	thiophosphonoacetate	5-methyluridine
L30	I	thiophosphonoacetate	5-methyluridine
L31	NH_2	thiophosphonoacetate	5-methyluridine
L32	H	thiophosphonoacetate	5-methyluridine
L33	OH	phosphorothioate	5-methyluridine
L34	OMe	phosphorothioate	5-methyluridine
L35	F	phosphorothioate	5-methyluridine
L36	Cl	phosphorothioate	5-methyluridine
L37	Br	phosphorothioate	5-methyluridine
L38	I	phosphorothioate	5-methyluridine
L39	NH_2	phosphorothioate	5-methyluridine
L40	H	phosphorothioate	5-methyluridine
L41	OH	phosphorodithioate	5-methyluridine
L42	OMe	phosphorodithioate	5-methyluridine
L43	F	phosphorodithioate	5-methyluridine
L44	Cl	phosphorodithioate	5-methyluridine
L45	Br	phosphorodithioate	5-methyluridine
L46	I	phosphorodithioate	5-methyluridine
L47	NH_2	phosphorodithioate	5-methyluridine
L48	H	phosphorodithioate	5-methyluridine
L49	OH	methylphosphonate	5-methyluridine
L50	OMe	methylphosphonate	5-methyluridine
L51	F	methylphosphonate	5-methyluridine
L52	Cl	methylphosphonate	5-methyluridine
L53	Br	methylphosphonate	5-methyluridine
L54	I	methylphosphonate	5-methyluridine
L55	NH_2	methylphosphonate	5-methyluridine
L56	H	methylphosphonate	5-methyluridine
L57	OH	boranophosphonate	5-methyluridine
L58	OMe	boranophosphonate	5-methyluridine
L59	F	boranophosphonate	5-methyluridine
L60	Cl	boranophosphonate	5-methyluridine
L61	Br	boranophosphonate	5-methyluridine
L62	I	boranophosphonate	5-methyluridine

TABLE 2-continued

Exemplary modified nucleotides contained in a synthetic guide sequence.



R_1 = OH or 2′modificiation
R_2 = OH or internucleotide linkage
B = base

#	R_1	R_2	B
L63	NH_2	boranophosphonate	5-methyluridine
L64	H	boranophosphonate	5-methyluridine

As described herein, certain unnatural base pairs (e.g., isoG and isoC, Z base and P base; see Zhang et al. (2015) *J. Am. Chem. Soc.*) may be advantageous for affecting the thermostability of the guide RNA secondary structure. These modifications can be used to prevent misfolding of the guide RNA scaffold with other domains of a guide RNA sequence.

Recent guide RNA:Cas9 protein structural information (FIG. **10**, as reported in Jiang et al. 2015, *Science*) and in vivo/in vitro functional mutation studies (see, e.g., Briner et al. 2014, *Mol. Cell,* 56, 333-9) indicate that the guide RNA scaffold is predominantly structurally conserved. This reinforces the importance of correct folding of the conserved domain of guide RNAs for functionality with Cas9. FIG. **10** shows the guide RNA scaffold secondary structure, displaying interactions with amino acids of Cas9. Most of the guide RNA nitrogenous bases are not involved in binding interactions with Cas9 protein.

The flanking sequences of the sgRNA scaffold increase the likelihood of misfolding and hence misfunction. The 20 nt guide targeting sequence, 5' of the scaffold region, is user-specified for each target, thus the likelihood of misfolding is variable or target-specific. Also, many emerging CRISPR-Cas applications append functional sequences 3' of the scaffold, such as CRISPRdisplay (Schechner et al., *Nat. Methods* 2015) and CRISPR-i/-a (Chen et al., *Cell* 2013), which are riboswitches or aptamers that also need to correctly and independently fold to function properly. To ensure that each of the functional domains (i.e. targeting guide, scaffold, aptamer) of a given sgRNA folds in a modular, independent manner, the structurally conserved scaffold base pairs can be substituted with unnatural, orthogonal base pairs (e.g., isoG and isoC; Z base and P base), and in some embodiments, substituted exclusively with unnatural, orthogonal base pairs. This ensures that the sgRNA scaffold sequences will not stably interact in a secondary structure with elements of the target-pairing guide sequence or other non-native domains incorporated in the guide RNA such as any aptamer sequences or any non-native 5' or 3' overhangs on the guide RNA. Alternatively, the unnatural, orthogonal base pairs mentioned above could be incorporated in any non-native overhangs or aptamers that may be present, thus to prevent secondary structures involving misfolding of the scaffold sequence(s).

B. Guide RNA with at Least One Modification

In one aspect, the present technology provides a guide RNA having at least one modification, constituting a modified gRNA.

In certain embodiments, the modified gRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19,

20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified nucleotides. In other embodiments, the modified gRNA comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified nucleotides. In certain embodiments, all nucleotides are modified. In certain embodiments, all the modifications are the same. In certain embodiments, all the modified nucleotides have the same type of modification. In certain embodiments, the modified gRNA comprises a combination of differently modified nucleotides. In certain embodiments, the modified gRNA comprises two or more modified nucleotides. In certain embodiments, the modified gRNA comprises three or more modified nucleotides. In certain embodiments, the modified nucleotides are arranged contiguously. In certain embodiments, the modified gRNA comprises at least one contiguous stretch of modified nucleotides. In certain embodiments, the modified gRNA comprises a contiguous stretch of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified nucleotides. Each modified nucleotide may independently comprise one or more types of modifications. In certain embodiments, no modified nucleotides are contiguous, or some but not all are contiguous, in the sequence of the modified gRNA.

In certain embodiments, the modification is within the 5' portion of the guide RNA. In certain embodiments, the modification is within the first five (5) nucleotides of the 5' portion of the guide RNA. In certain embodiments, the modification is within the first three (3) nucleotides of the 5' portion of the guide RNA. In certain embodiments, the modification is within the 3' portion of the guide RNA. In certain embodiments, the modification is within the last five (5) nucleotides of the 3' portion of the guide RNA. In certain embodiments, the modification is within the last three (3) nucleotides of the 3' portion of the guide RNA. In certain embodiments, the modification is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA.

In certain embodiments, the modification is incorporated in the 5' portion or the 3' portion of the guide RNA, particularly within the first 5 or 10 nucleotides of the 5' portion or within the last 5 or 10 nucleotides of the 3' portion to, for example, protect the RNA from degradation by nucleases or for other purposes. In some other embodiments, the modification is in both the 5' portion and the 3' portion of the guide RNA, particularly within the first 5 or 10 nucleotides of the 5' portion and within the last 5 or 10 nucleotides of the 3' portion to, for example, protect the RNA from degradation by nucleases or for other purposes. In certain embodiments, more than one type of modification is present in both the 5' portion and the 3' portion of the guide RNA. In certain embodiments, the modifications are located at the 5' end, at the 3' end, and within the internal sequence of the guide RNA. In certain embodiments, a guide RNA comprises 40 or fewer, alternatively 20 or fewer, alternatively 15 or fewer, alternatively 10 or fewer, alternatively 5 or fewer, alternatively 3 or fewer deoxyribonucleotide residues in the 5' or 3' portion of the guide RNA.

In certain embodiments, the modification is within the crRNA segment of the guide RNA. In certain embodiments, the modification is within the guide sequence of the crRNA. In certain embodiments, the modification is within the first five (5) nucleotides of the crRNA segment. In certain embodiments, the modification is within the first three (3) nucleotides of the crRNA segment. In certain embodiments, the modification is within a 5'-overhang on the crRNA segment. In certain embodiments, the modification is within the tracrRNA segment of the guide RNA. In certain embodiments, the modification is within the last five (5) nucleotides of the tracrRNA segment of the guide RNA. In certain embodiments, the modification is within the last three (3) nucleotides of the tracrRNA segment of the guide RNA. In certain embodiments, when the guide RNA is a single guide RNA, the modification is located within the loop of the guide RNA. In certain embodiments, one or more modifications is within the loop L region. In certain embodiments, the modification comprises a dye, a non-fluorescent label, or a tag conjugated to a linker incorporated between two nucleotides as described above, for example by conjugation to a 2-(3-(dye/label/tag-amido)propanamido)propane-1,3-diol bis(phosphodiester) linker or to a modified base of a nucleotide in the loop or L region.

In certain embodiments, the modification comprises an end modification, such as a 5' end modification or a 3' end modification. Examples of end modifications include, but are not limited to phosphorylation (as natural phosphate or polyphosphate or as modified phosphohate groups such as for example, alkylphosphonate, phosphonocarboxylate, phosphonoacetate, boranophosphonate, phosphorothioate, phosphorodithioate and the like), biotinylation, conjugating or conjugated molecules, linkers, dyes, labels, tags, functional groups (such as for example but not limited to 5'-amino, 5'-thio, 5'-amido, 5'carboxy and the like), inverted linkages, or hydrocarbon moieties which may comprise ether, polyethylene glycol (PEG), ester, hydroxyl, aryl, halo, phosphodiester, bicyclic, heterocyclic or other organic functional group. In certain embodiments, the end modification comprises dimethoxytrityl.

In certain embodiments, the modification comprises a modified base. As used herein, "unmodified" bases include the purine bases adenine (A) and guanine (G), and the pyrimidine bases thymine (T), cytosine (C) and uracil (U). Examples of modified bases include, but are not limited to, synthetic and natural bases such as 2-thioU, 2-thioC, 4-thioU, 6-thioG, 2-aminoA, 2-aminoP, pseudouracil, hypoxanthine, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-methylC, 5-methylU, 5-hydroxymethylcytosine, 5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil, 5-allylU, 5-allylC, 5-aminoallyl-uracil, and 5-aminoallyl-cytosine. In certain embodiments, the modification comprises an abasic nucleotide. In certain embodiments, the modification comprises a nonstandard purine or pyrimidine structure, such as Z or P, isoC or isoG, UNA, 5-methylpyrymidine, x(A,G,C,T) or y(A,G,C,T). In certain embodiments, the modified gRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified bases. In other embodiments, the modified gRNA comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified bases. In certain embodiments, all bases in a gRNA are modified.

In certain embodiments, the modification comprises a modified sugar. Examples of modified sugars include, but are not limited to, sugars having modifications at the 2' position or modifications at the 4' position. For example, in certain embodiments, the sugar comprises 2'-O—C_{1-4}alkyl, such as 2'-O-methyl (2'-OMe). In certain embodiments, the sugar comprises 2'-O—C_{1-3}alkyl-O—C_{1-3}alkyl, such as 2'-methoxyethoxy (2'-O—$CH_2CH_2OCH_3$) also known as 2'-O-(2-methoxyethyl) or 2'-MOE. In certain embodiments, the sugar comprises 2'-halo, such as 2'-F, 2'-Br, 2'-Cl, or 2'-I.

In certain embodiments, the sugar comprises 2'-NH_2. In certain embodiments, the sugar comprises 2'-H (e.g., a deoxynucleotide). In certain embodiments, the sugar comprises 2'-arabino or 2'-F-arabino. In certain embodiments, the sugar comprises 2'-LNA or 2'-ULNA. In certain embodiments, the sugar comprises a 4'-thioribosyl. In certain embodiments, the modified gRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified sugars. In other embodiments, the modified gRNA comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified sugars. In certain embodiments, all sugars in a gRNA are modified.

In certain embodiments, the modification comprises a modified backbone (i.e., an internucleotide linkage other than a natural phosphodiester). Examples of modified internucleotide linkages include, but are not limited to, a phosphorothioate internucleotide linkage, a chiral phosphorothioate internucleotide linkage, a phosphorodithioate internucleotide linkage, a boranophosphonate internucleotide linkage, a C_{1-4}alkyl phosphonate internucleotide linkage such as a methylphosphonate internucleotide linkage, a boranophosphonate internucleotide linkage, a phosphonocarboxylate internucleotide linkage such as a phosphonoacetate internucleotide linkage, a phosphonocarboxylate ester internucleotide linkage such as a phosphonoacetate ester internucleotide linkage, a thiophosphonocarboxylate internucleotide linkage such as for example a thiophosphonoacetate internucleotide linkage, a thiophosphonocarboxylate ester internucleotide linkage such as a thiophosphonoacetate ester internucleotide linkage. Various salts, mixed salts and free acid forms are also included. In certain embodiments, the modified gRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified internucleotide linkages. In other embodiments, the modified gRNA comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified internucleotide linkages. In certain embodiments, all internucleotide linkages in a gRNA are modified.

In certain embodiments, the modification is a 2'-O—C_{1-4}alkyl, 2'-H, 2'-O—C_{1-3}alkyl-O—C_{1-3}alkyl, 2'-F, 2'-NH_2, 2'-arabino, 2'-F-arabino, 2'-LNA, 2'-ULNA, 4'-thioribosyl, 2-thioU, 2-thioC, 4-thioU, 6-thioG, 2-aminoA, 2-aminoP, pseudouracil, hypoxanthine, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-MeC, 5-MeU, 5-hydroxymethylcytosine, 5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil, 5-allylU, 5-allylC, 5-aminoallyl-uracil, 5-aminoallyl-cytosine, an abasic nucleotide, Z, P, UNA, isoC, isoG, 5-methyl-pyrimidine, x(A,G,C,T), y(A,G,C,T), a 3'-phosphorothioate group, a 3'-phosphonoacetate group, a 3'-phosphonoacetate ester group, a 3'-thiophosphonoacetate group, a 3'-thiophosphonoacetate ester group, a 3'-methylphosphonate group, a 3'-boranophosphonate group, a 3'-phosphorodithioate group, or combinations thereof.

In certain embodiments, the modified nucleotide comprises a 2'-O-methyl-3'-phosphorothioate. In certain embodiments, the modified nucleotide comprises a 2'-O-methyl-3'-phosphonoacetate. In certain embodiments, the modified nucleotide comprises a 2'-O-methyl-3'-thiophosphonoacetate. In certain embodiments, the modified nucleotide comprises a Z base. In certain embodiments, the modified nucleotide comprises a 2'-halo-3'-phosphorothioate. In certain embodiments, the modified nucleotide comprises a 2'-halo-3'-phosphonoacetate. In certain embodiments, the modified nucleotide comprises a 2'-halo-3'-thiophosphonoacetate. In certain embodiments, the modified nucleotide comprises a 2'-fluoro-3'-phosphorothioate. In certain embodiments, the modified nucleotide comprises a 2'-fluoro-3'-phosphonoacetate. In certain embodiments, the modified nucleotide comprises a 2'-fluoro-3'-thiophosphonoacetate.

In certain embodiments, the guide RNA comprises an oligonucleotide represented by Formula (I):

$$W—Y \text{ or } Y—W \quad (I)$$

wherein W represents a nucleotide or a stretch of nucleotides of the oligonucleotide comprising at least one modification and Y represents an unmodified portion of the oligonucleotide.

In certain embodiments, W is within the 5' portion of the guide RNA. In certain embodiments, W is at least partially within the first five (5) nucleotides of the 5' portion of the guide RNA. In certain embodiments, W is at least partially within the first three (3) nucleotides of the 5' portion of the guide RNA. In certain embodiments, W is within the 3' portion of the guide RNA. In certain embodiments, W is at least partially within the last five (5) nucleotides of the 3' portion of the guide RNA. In certain embodiments, W is at least partially within the last three (3) nucleotides of the 3' portion of the guide RNA. In certain embodiments, W is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA.

In certain embodiments, W comprises an end modification, such as a 5' end modification or a 3' end modification as described above. In certain embodiments, the end modification comprises dimethoxytrityl.

In certain embodiments, W comprises a modified base as described above. In certain embodiments, W comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified bases. In other embodiments, W comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified bases. In certain embodiments, all bases in a gRNA are modified.

In certain embodiments, W comprises a modified sugar as described above. In certain embodiments, W comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified sugars. In other embodiments, W comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified sugars. In certain embodiments, all sugars in a gRNA are modified.

In certain embodiments, W comprises a modified backbone (i.e., an internucleotide linkage other than a phosphodiester) as described above. In certain embodiments, W comprises more than one, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 modified internucleotide linkages. In other embodiments, W comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified internucleotide linkages. In certain embodiments, all internucleotide linkages in a gRNA are modified.

In certain embodiments, W comprises a 2'-O—C_{1-4}alkyl, 2'-H, 2'-O—C_{1-3}alkyl-O—C_{1-3}alkyl, 2'-F, 2'-NH_2, 2'-arabino, 2'-F-arabino, 2'-LNA, 2'-ULNA, 4'-thioribosyl, 2-thioU, 2-thioC, 4-thioU, 6-thioG, 2-aminoA, 2-aminoP,

pseudouracil, hypoxanthine, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-MeC, 5-MeU, 5-hydroxymethylcytosine, 5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil, 5-allylU, 5-allylC, 5-aminoallyl-uracil, 5-aminoallyl-cytosine, abasic nucleotides, Z, P, UNA, isoC, isoG, 5-methyl-pyrimidine, x(A,G,C,T), y(A,G,C,T), a phosphorothioate internucleotide linkage, a phosphonoacetate internucleotide linkage, a phosphonoacetate ester internucleotide linkage, a thiophosphonoacetate internucleotide linkage, a thiophosphonoacetate ester internucleotide linkage a methylphosphonate internucleotide linkage, a boranophosphonate internucleotide linkage, a phosphorodithioate internucleotide linkage, or combinations thereof.

In certain embodiments, W comprises a 2'-O-methyl and a 3'-phosphorothioate group on the same nucleotide. In certain embodiments, W comprises a 2'-O-methyl and a 3'-phosphonoacetate group on the same nucleotide. In certain embodiments, W comprises a 2'-O-methyl and 3[1]-thiophosphonoacetate group on the same nucleotide. In certain embodiments, W comprises a 2'-F and a 3'-phosphorothioate group on the same nucleotide. In certain embodiments, W comprises a 2'-F and a 3'-phosphonoacetate group on the same nucleotide. In certain embodiments, W comprises a 2'-F and 3[1]-thiophosphonoacetate group on the same nucleotide.

In certain embodiments, W comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 modified nucleotides. In certain embodiments, each of the modified nucleotides comprises the same modification. In certain embodiments, W comprises a combination of variously modified nucleotides. In certain embodiments, W comprises two or more modified nucleotides. In certain embodiments, W comprises three or more modified nucleotides. In certain embodiments, the modified nucleotides are not arranged contiguously in the sequence, or at least not entirely, as one or more unmodified nucleotides may intercede. In certain embodiments, the modified nucleotides are arranged contiguously. In certain embodiments, W comprises at least one contiguous stretch of modified nucleotides. In certain embodiments, W comprises a contiguous stretch of at least three (3) modified nucleotides. In certain embodiments, W comprises a contiguous stretch of at least four (4) modified nucleotides. In certain embodiments, W comprises a contiguous stretch of at least five (5) modified nucleotides.

In certain embodiments, the guide RNA comprises an oligonucleotide represented by Formula (II):

$$M_mN_n \quad \text{(II)}$$

wherein each N independently represents an unmodified ribonucleotide;

wherein each M represents a modified nucleotide and is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 3'-P(S) ribonucleotide, a 3'-PACE ribonucleotide, a 3'-thioPACE ribonucleotide, a 2'-O-methyl-3'-P(S)-ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, a Z nucleotide, and a 2'-deoxynucleotide;

wherein each M is at any position of the sequence of the guide RNA;

wherein any given M is the same or different from any other M, and any given N is the same or different from any other N; and

wherein each of m and n are independently selected from an integer between 0 and 219, provided that $50<m+n\leq220$, and m is not 0.

In some embodiments, $m+n<150$.

In certain embodiments, each M is modified with one or more moieties independently selected from the group consisting of 2'-F, 2-thiouracil, 4-thiouracil, 2-aminoadenine, hypoxanthine, 5-methylcytosine, 5-methyluracil, 5-allylaminouracil, squarate linkage, a triazolo linkage, and a 2-(4-butylamidofluorescein)propane-1,3-diol bis(phosphodiester) linkage. In some embodiments, M comprises a dye attached through a linker.

In certain embodiments, each M is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, and a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M is independently selected from the group consisting of a 2'-O-methyl-3'-PACE ribonucleotide and a 2'-O-methyl-3'-thioPACE ribonucleotide.

In certain embodiments, where $m>1$, any given M is the same or different from any other M. In certain embodiments, where $m>1$, each M has the same modification.

In certain embodiments, each M is a 2'-O-methyl-3'-PACE ribonucleotide, m is selected from an integer between 1 and 10, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided $50<m+n\leq150$. In certain embodiments, each M is a 2'-O-methyl-3'-PACE ribonucleotide, m is selected from an integer between 1 and 5, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided $50<m+n\leq150$. In certain embodiments, each M is a 2'-O-methyl-3'-PACE ribonucleotide, m is selected from an integer between 2 and 5, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 148, provided $50<m+n\leq150$. In certain embodiments, m is 1. In certain embodiments, m is 2. In certain embodiments, m is 3. In certain embodiments, m is 4. In certain embodiments, m is 5.

In certain embodiments, each M is a 2'-O-methyl-3'-thioPACE ribonucleotide, m is selected from an integer between 1 and 10, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided $50<m+n\leq150$. In certain embodiments, each M is a 2'-O-methyl-3'-thioPACE ribonucleotide, m is selected from an integer between 1 and 5, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided $50<m+n\leq150$. In certain embodiments, each M is a 2'-O-methyl-3'-thioPACE ribonucleotide, m is selected from an integer between 2 and 5, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 148, provided $50<m+n\leq150$. In certain embodiments, m is 1. In certain embodiments, m is 2. In certain embodiments, m is 3. In certain embodiments, m is 4. In certain embodiments, m is 5.

In certain embodiments, each M is a 2'-O-methyl ribonucleotide, m is selected from an integer between 1 and 40, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided $50<m+n\leq150$. In certain embodiments, each M is a 2'-O-methyl ribonucleotide, m is selected from an integer between 1 and 25, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided $50<m+n\leq150$. In certain embodiments, each M is a 2'-O-methyl ribonucleotide, m is selected from an integer

between 1 and 20, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided 50<m+n≤150. In certain embodiments, m is 1. In certain embodiments, m is 2. In certain embodiments, m is 3. In certain embodiments, m is 4. In certain embodiments, m is 5. In certain embodiments, m is 10. In certain embodiments, m is 15. In certain embodiments, m is 20. In certain embodiments, m is 30. In certain embodiments, m is 40.

In certain embodiments, each M is a 2'-deoxynucleotide, m is selected from an integer between 1 and 30, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided 50<m+n≤150. In certain embodiments, each M is 2'-deoxynucleotide, m is selected from an integer between 1 and 20, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided 50<m+n≤150. In certain embodiments, m is 5. In certain embodiments, m is 10. In certain embodiments, m is 15. In certain embodiments, m is 20. In certain embodiments, m is 30.

In certain embodiments, each M is a 2'-O-methyl-3'-P(S) ribonucleotide, m is selected from an integer between 1 and 10, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided 50<m+n≤150. In certain embodiments, each M is a 2'-O-methyl-3'-P(S) ribonucleotide, m is selected from an integer between 1 and 5, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided 50<m+n≤150. In certain embodiments, m is 1. In certain embodiments, m is 2. In certain embodiments, m is 3. In certain embodiments, m is 4. In certain embodiments, m is 5.

In certain embodiments, each M is a Z nucleotide, m is selected from an integer between 1 and 10, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided 50<m+n≤150. In certain embodiments, each M is a Z nucleotide, m is selected from an integer between 1 and 5, each N is independently selected from the group consisting of A, U, C, and G, and n is selected from an integer between 1 and 149, provided 50<m+n≤150. In certain embodiments, m is 1. In certain embodiments, m is 2. In certain embodiments, m is 3. In certain embodiments, m is 4. In certain embodiments, m is 5.

In certain embodiments, the modification is a stability-altering modification. In certain embodiments, the modification increases nuclease resistance of the guide RNA relative to a guide RNA without the modification, thus it enhances the guide RNA stability. In certain embodiments, the stability-altering modification is a stability-enhancing modification. For example, in certain embodiments, the stability-enhancing modification comprises a 2'-O-methyl or a 2'-O—C_{1-4}alkyl nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-halo nucleotide, such as 2'-F, 2'-Br, 2'-Cl, or 2'-I. In certain embodiments, the stability-enhancing modification comprises a 2'MOE or a 2'-O—C_{1-3}alkyl-O—C_{1-3}alkyl. In certain embodiments, the stability-enhancing modification comprises a 2'-NH_2 nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-H (or 2'-deoxy) nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-arabino or a 2'-F-arabino. In certain embodiments, the stability-enhancing modification comprises a 4'-thioribosyl sugar moiety. In certain embodiments, the stability-enhancing modification comprises a 3'-phosphorothioate group. In certain embodiments, the stability-enhancing modification comprises a 3'-phosphonoacetate group. In certain embodiments, the stability-enhancing modification comprises a nucleotide containing a 3'-thiophosphonoacetate group. In certain embodiments, the stability-enhancing modification comprises a nucleotide containing a 3'-methylphosphonate group. In certain embodiments, the stability-enhancing modification comprises a nucleotide containing a 3'-boranophosphate group. In certain embodiments, the stability-enhancing modification comprises a nucleotide containing a 3'-phosphorodithioate group. In certain embodiments, the stability-enhancing modification comprises a locked nucleic acid ("LNA") nucleotide. In certain embodiments, the stability-enhancing modification comprises an unlocked nucleic acid ("ULNA") nucleotide.

In certain embodiments, the stability-enhancing modification comprises a 2'-O-methyl and a 3'-phosphorothioate group on the same nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-O-methyl and a 3'-phosphonoacetate group on the same nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-O-methyl and a 3'-thiophosphonoacetate group on the same nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-fluoro and a 3'-phosphorothioate group on the same nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-fluoro and a 3'-phosphonoacetate group on the same nucleotide. In certain embodiments, the stability-enhancing modification comprises a 2'-fluoro and a 3'-thiophosphonoacetate group on the same nucleotide.

In certain embodiments, the modification is a specificity-altering modification. In some embodiments, specificity enhancement may be achieved by enhancing on-target binding and/or cleavage, or reducing off-target binding and/or cleavage, or a combination of both. In some other embodiments, specificity reduction may be achieved, for example, by reducing on-target binding and/or cleavage, or increasing off-target binding and/or cleavage, or a combination of both.

In certain embodiments, the specificity-altering modification comprises a 2'-O-methyl. In certain embodiments, the specificity-altering modification comprises a 2'-halo, such as 2'-fluoro.

In certain embodiments, the specificity-altering modification comprises a 2-thiouracil base (2-thioU). In certain embodiments, the specificity-altering modification comprises 2-thioC. In certain embodiments, the specificity-altering modification comprises 4-thioU. In certain embodiments, the specificity-altering modification comprises 6-thioG. In certain embodiments, the specificity-altering modification comprises 2-aminoA. In certain embodiments, the specificity-altering modification comprises a 2-aminopurine. In certain embodiments, the specificity-altering modification comprises pseudouracil. In certain embodiments, the specificity-altering modification comprises hypoxanthine. In certain embodiments, the specificity-altering modification comprises 7-deazaguanine. In certain embodiments, the specificity-altering modification comprises 7-deaza-8-azaguanine. In certain embodiments, the specificity-altering modification comprises 7-deazaadenine. In certain embodiments, the specificity-altering modification comprises 7-deaza-8-azaadenine. In certain embodiments, the specificity-altering modification comprises 5-methylC. In certain embodiments, the specificity-altering modification comprises 5-methylU. In certain embodiments, the specificity-altering modification comprises 5-hydroxymethylcytosine. In certain embodiments, the specificity-altering modification

comprises 5-hydroxymethyluracil. In certain embodiments, the specificity-altering modification comprises 5,6-dehydrouracil. In certain embodiments, the specificity-altering modification comprises 5-propynylcytosine. In certain embodiments, the specificity-altering modification comprises 5-propynyluracil. In certain embodiments, the specificity-altering modification comprises 5-ethynylcytosine. In certain embodiments, the specificity-altering modification comprises 5-ethynyluracil. In certain embodiments, the specificity-altering modification comprises 5-allylU. In certain embodiments, the specificity-altering modification comprises 5-allylC. In certain embodiments, the specificity-altering modification comprises 5-aminoallylU. In certain embodiments, the specificity-altering modification comprises 5-aminoallylC. In certain embodiments, the specificity-altering modification comprises an abasic nucleotide. In certain embodiments, the specificity-altering modification comprises a Z base. In certain embodiments, the specificity-altering modification comprises P base. In certain embodiments, the specificity-altering modification comprises a UNA base. In certain embodiments, the specificity-altering modification comprises isoC. In certain embodiments, the specificity-altering modification comprises isoG. In certain embodiments, the specificity-altering modification comprises 5-methyl-pyrimidine. In certain embodiments, the specificity-altering modification comprises x(A,G,C,T). In certain embodiments, the specificity-altering modification comprises y(A,G,C,T).

In certain embodiments, the specificity-altering modification comprises a phosphorothioate internucleotide linkage. In certain embodiments, the specificity-altering modification comprises a phosphonoacetate internucleotide linkage. In certain embodiments, the specificity-altering modification comprises a thiophosphonoacetate internucleotide linkage. In certain embodiments, the specificity-altering modification comprises a methylphosphonate internucleotide linkage. In certain embodiments, the specificity-altering modification comprises a boranophosphate internucleotide linkage. In certain embodiments, the specificity-altering modification comprises a phosphorodithioate internucleotide linkage. In certain embodiments, the specificity-altering modification comprises a ULNA. In certain embodiments, the specificity-altering modification comprises an LNA.

In certain embodiments, the modification alters RNA base pairing by, for example, altering the melting temperature (Tm) of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification lowers the Tm of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification raises the Tm of the guide RNA relative to a guide RNA without the modification.

In certain embodiments, the specificity-altering modification lowers the Tm of a base pairing interaction. In certain embodiments, the modification that lowers the Tm of the base pairing interaction is a 2'-deoxy, as it is well-known in the art that DNA/DNA base pairs have lower Tm than their respective counterpart in RNA/DNA duplexes. In certain embodiments, the modification that lowers the Tm of the base pairing interaction is 2-thiouracil, which slightly lowers Tm of G-U wobble pair. In certain embodiments, the modification that lowers the Tm of the base pairing interaction is a phosphorothioate internucleotide linkage or a phosphorodithioate internucleotide linkage, which lower the Tm by ~0.5° C. per modification. In certain embodiments, the modification that lowers the Tm of the base pairing interaction is a boranophosphonate internucleotide linkage, which lowers the Tm by ~0.5-0.8° C. per modification. In certain embodiments, the modification that lowers the Tm of the base pairing interaction is a phosphonoacetate internucleotide linkage, which lowers the Tm by ~1.3° C. per modification. In certain embodiments, the modification that lowers the Tm of the base pairing interaction is unlocked nucleic acid ("ULNA"), which lowers the Tm by ~5-8° C. per modification. In certain embodiments, the modification that lowers the Tm of the base pairing interaction is 2'-O-methyl-3'-methylphosphonate.

In certain embodiments, the specificity-altering modification raises the Tm of a base pairing interaction. In certain embodiments, the modification that raises the Tm of the base pairing interaction is a 2'-O-methyl, which raises Tm by ~0.5-0.7° C. per modification. In certain embodiments, the modification that raises the Tm of the base pairing interaction is a 2'-F, which raises Tm by ~1° C. per modification. In certain embodiments, the modification that raises the Tm of the base pairing interaction is a 2-thiouracil, which raises Tm of A-U pair (and, as noted above, slightly lowers Tm of G-U wobble pair). In certain embodiments, the modification that raises the Tm of the base pairing interaction is a 4-thiouracil, which raises Tm of G-U wobble pair and slightly raises Tm of A-U pair. In certain embodiments, the modification that raises the Tm of the base pairing interaction is a 2-amino-adenine, which raises Tm of its base pairing with U by ~1° C. per modification. In certain embodiments, the modification that raises the Tm of the base pairing interaction is a 5-methyl-uracil (5-methylU) (see, e.g., Wang & Kool (1995) *Biochemistry,* 34, 4125-32). In certain embodiments, the modification that raises the Tm of the base pairing interaction is a 5-methyl-cytosine (5-methylC). In certain embodiments, the modification that raises the Tm of the base pairing interaction is a locked nucleic acid ("LNA"), which raises Tm by 2-10° C. per modification.

In certain embodiments, the modification alters transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification increases transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification decreases transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification neutralizes the anionic charge on phosphate to allow passive diffusion into cells. In certain embodiments, the charge-neutralizing modification comprises a phosphonoacetate alkyl ester internucleotide linkage, such as a phosphonoacetate methyl ester internucleotide linkage.

In certain embodiments, the modification alters the immunostimulatory effect of the guide RNA relative to a guide RNA without the modification. It was initially discovered that unmethylated bacterial DNA and synthetic analogs thereof are ligands for TLR9 (see Hemmi et al. (2000) *Nature,* 408, 740-5). The stimulation of TLR9 can be mitigated in the dinucleotide motif for example by modifying the C and G residues. The use of 5-methylcytosine, 2-aminocytosine, 2-thiocytosine, 5-methylisocytosine, P nucleobase (6-(β-D-2'-Deoxyribofuranosyl)-3,4-dihydro-8H-pyrimido[4,5-c][1,2]oxazin-7-one), and 2'-O-methylcytosine all result in loss or decrease in TLR9 stimulation. In certain embodiments, use of 6-thioguanine, 2,6-diaminopurine, 2-aminopurine, xanthosine, inosine, 7-deazaxanthosine, isoguanine, 8-oxoguanine, nebularine, 8-bromoguanine, K-nucleobase (2-amino-N-methoxyadenosine), and/or 2'-O-methylguanine can result in loss or decrease in TLR9 stimulation. In some embodiments, use of phosphodiester

modifications can lower or eliminate the TLR9 response. Typically, synthetically incorporated phosphorothioates can decrease the TLR9 response to a limited extent, as is thought to result from the presence of two stereoisomers of each phosphorothioate in synthetic RNA. However, it has been shown that phosphorothioate-modified DNA lacking CpG motifs stimulate TLR9 to a rather small extent. The negative charge on the phosphorus is an important element for recognition by TLR9 and therefore removing the negative charge using alkylphosphonates can result in loss or decrease in TLR9 stimulation. The use of phosphonoacetate (PACE) internucleotide linkages between deoxynucleosides in 5' and 3' terminal sequences can significantly increase the TLR9 response; however, the use of thiophosphonoacetate (thioPACE) internucleotide linkages between deoxynucleosides in 5' and 3' terminal sequences can result in loss or decrease in TLR9 stimulation. In certain embodiments, use of sugar modifications that the favor C3'-endo conformation such as 2'-O-methyl modifications can be incorporated at 5' and 3' termini to decrease the TLR9 response. TLR 7 and TLR8 can be stimulated by molecules containing 7-deazaguanine and by single-stranded RNA (see, e.g., Heil et al. (2004) *Science,* 303, 1526-9). TLR3 has been implicated in cellular immunoresponses to virus-derived double-stranded RNA. In certain embodiments, these TLR responses can be mitigated for example by using 2'-O-methyl modifications, modified phosphodiester linkages containing sulfur, or modifications that decrease internucleotide negative charge such as methylphosphonate and/or phosphonoacetate internucleotide linkages.

In certain embodiments, the modification enhances stability and specificity of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification enhances stability and transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification enhances specificity and transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, the modification enhances the overall efficacy of the guide RNA relative to a guide RNA without the modification.

C. Guide RNA with a Combination of Modifications

In one aspect, the present technology provides a guide RNA having a combination of two or more modifications.

In certain embodiments, the two modifications are on the same nucleotide (for example, one nucleotide comprises a 2'-O-methyl and a 3'-thiophosphonoacetate moiety). In other embodiments, the two modifications are on two different nucleotides (for example, one nucleotide has a 2-thioU base and another nucleotide has a 2'-O-methyl group).

In certain embodiments, each modification in the guide RNA is the same. In certain embodiments, at least one modification in the guide RNA is different from at least one other modification in the guide RNA. In certain embodiments, a single nucleotide within the guide RNA possesses two or more modifications.

In certain embodiments, the guide RNA comprises a combination of different types of modifications, and at least one type in the combination exists in multiple places in the guide RNA In certain embodiments, at least one type in the combination appears 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 times in the guide RNA.

In certain embodiments, at least one type of the modifications in the combination appears in two or more modified nucleotides. In certain embodiments, at least one type of the modifications in the combination appears in three or more modified nucleotides. In certain embodiments, the modified nucleotides are not arranged contiguously in the sequence, or at least not entirely, as one or more unmodified nucleotides may intercede. In certain embodiments, the modified nucleotides are arranged contiguously. In certain embodiments, the guide RNA comprises a stretch of contiguous modified nucleotides of the same type. In certain embodiments, the stretch has at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 modified nucleotides.

In certain embodiments, at least one type of the modifications in the combination is within the 5' portion of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the first five (5) nucleotides of the 5' portion of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the first three (3) nucleotides of the 5' portion of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the 3' portion of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the last five (5) nucleotides of the 3' portion of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the last three (3) nucleotides of the 3' portion of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA.

In certain embodiments, at least one type of the modifications in the combination is incorporated in the 5' portion or 3' portion of the guide RNA, particularly within the first 5 or 10 nucleotides of the 5' portion or within the last 5 or 10 nucleotides of the 3' portion to, for example, protect the RNA from degradation by nucleases or for other purposes. In certain embodiments, at least one type of the modifications in the combination is in the 5' portion and at least one type of the modifications in the combination is in the 3' portion of the guide RNA, particularly within the first 5 or 10 nucleotides of the 5' portion and within the last 5 or 10 nucleotides of the 3' portion to, for example, protect the RNA from degradation by nucleases or for other purposes. In certain embodiments, a guide RNA comprises 20 or fewer, alternatively 15 or fewer, alternatively 15 or fewer, alternatively 10 or fewer, alternatively 5 or fewer, alternatively 3 or fewer deoxyribonucleotide residues in the 5' portion of the guide RNA.

In certain embodiments, at least one type of the modifications in the combination is within the crRNA segment of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the guide sequence of the crRNA. In certain embodiments, at least one type of the modifications in the combination is within the first five (5) nucleotides of the crRNA segment. In certain embodiments, at least one type of the modifications in the combination is within the first three (3) nucleotides of the crRNA segment. In certain embodiments, at least one type of the modifications in the combination is within the tracrRNA segment of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the last five (5) nucleotides of the tracrRNA segment of the guide RNA. In certain embodiments, at least one type of the modifications in the combination is within the last three (3) nucleotides of the tracrRNA segment of the guide RNA.

In certain embodiments, a first type of modification in the combination is within the 5' portion of the guide RNA and a second type of modification in the combination is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA. In certain embodiments, the first type of modification is within the first five (5) nucleotides of the 5' portion of the guide RNA. In certain embodiments, the first type of modification is within the first three (3) nucleotides of the 5' portion of the guide RNA.

In certain embodiments, a first type of modification in the combination is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA and a second type of modification in the combination is within the 3' portion of the guide RNA. In certain embodiments, the second type of modification is within the last five (5) nucleotides of the 3' portion of the guide RNA. In certain embodiments, the second type of modification is within the last three (3) nucleotides of the 3' portion of the guide RNA.

In certain embodiments, a first type of modification in the combination is within the 5' portion of the guide RNA and a second type of modification in the combination is within the 3' portion of the guide RNA. In certain embodiments, the first type of modification is within the first five (5) nucleotides of the 5' portion of the guide RNA. In certain embodiments, the first type of modification is within the first three (3) nucleotides of the 5' portion of the guide RNA. In certain embodiments, the second type of modification is within the last five (5) nucleotides of the 3' portion of the guide RNA. In certain embodiments, the second type of modification is within the last three (3) nucleotides of the 3' portion of the guide RNA.

In certain embodiments, a first type of modification in the combination is within the 5' portion of the guide RNA, a second type of modification in the combination is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA, and a third type of modification in the combination is within the 3' portion of the guide RNA. In certain embodiments, the first type of modification is within the first five (5) nucleotides of the 5' portion of the guide RNA. In certain embodiments, the first type of modification is within the first three (3) nucleotides of the 5' portion of the guide RNA. In certain embodiments, the third type of modification is within the last five (5) nucleotides of the 3' portion of the guide RNA. In certain embodiments, the third type of modification is within the last three (3) nucleotides of the 3' portion of the guide RNA.

In certain embodiments, a first type of modification in the combination is within the crRNA segment of the guide RNA and a second type of modification in the combination is within the tracr segment. In certain embodiments, the first type of modification is within the guide sequence of the crRNA. In certain embodiments, the first type of modification is within the first five (5) nucleotides of the crRNA segment. In certain embodiments, the first type of modification is within the first three (3) nucleotides of the crRNA segment. In certain embodiments, the second type of modification is within the last five (5) nucleotides of the tracrRNA segment of the guide RNA. In certain embodiments, the second type of modification is within the last three (3) nucleotides of the tracrRNA segment of the guide RNA.

In certain embodiments, a first type and a second type of modification in the combination are within the crRNA segment of the guide RNA. In certain embodiments, the first type of modification is within the guide sequence of the crRNA. In certain embodiments, the first type of modification is within the first five (5) nucleotides of the crRNA segment. In certain embodiments, the first type of modification is within the first three (3) nucleotides of the crRNA segment.

In certain embodiments, a first type and a second type of modification in the combination are within the crRNA segment of the guide RNA and a third type of modification in the combination is within the tracr segment. In certain embodiments, the first type of modification is within the guide sequence of the crRNA. In certain embodiments, the first type of modification is within the first five (5) nucleotides of the crRNA segment. In certain embodiments, the first type of modification is within the first three (3) nucleotides of the crRNA segment. In certain embodiments, the third type of modification is within the last five (5) nucleotides of the tracrRNA segment of the guide RNA. In certain embodiments, the third type of modification is within the last three (3) nucleotides of the tracrRNA segment of the guide RNA.

In certain embodiments, at least one of the modifications in the combination comprises an end modification, such as a 5' end modification or a 3' end modification as described above. In certain embodiments, the end modification comprises dimethoxytrityl.

In certain embodiments, at least one of the modifications in the combination comprises a modified base. In certain embodiments, the modified gRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 modified bases. In other embodiments, the modified gRNA comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified bases. In certain embodiments, all bases in a gRNA are modified.

In certain embodiments, at least one of the modifications in the combination comprises a modified sugar. In certain embodiments, the modified gRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 modified sugars. In other embodiments, the modified gRNA comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified sugars. In certain embodiments, all sugars in a gRNA are modified.

In certain embodiments, at least one of the modifications in the combination comprises a modified backbone (i.e., an internucleotide linkage other than a natural phosphodiester). In certain embodiments, the modified gRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 modified internucleotide linkages. In other embodiments, the modified gRNA comprises at least 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130 or 140 modified internucleotide linkages. In certain embodiments, all internucleotide linkages in a gRNA are modified.

In certain embodiments, at least one of the modifications in the combination comprises a 2'-O-methyl, a 2'-fluoro, a 2'-amino, a 2'-deoxy, a 2'-arabino, a 2'-F-arabino, a 2-thiouracil, a 2-aminoadenine, a 5-methylcytosine, a 5-aminoallyluracil, a Z base, a 3'-phosphorothioate, a 3'-phosphonoacetate, a 3'-phosphonoacetate ester, a 3'-thiophosphonoacetate, a 3'-thiophosphonoacetate ester, a 3'-methylphosphonate, a 3'-boranophosphonate, a 3'-phosphorodithioate, or combinations thereof. In certain embodiments, at least one of the modifications in the combination comprises a 2'-O-methyl, a 2'-deoxy, a Z base, a phosphorothioate internucleotide linkage, a phosphonoacetate internucleotide linkage, a thiophosphonoacetate internucleotide linkage, or combinations thereof. In certain embodiments, at least one of the modifications in the combination comprises a 2'-F, a

2-thioU, a 4-thioU, a 2-aminoA, a 5-methylC, a 5-methylU, a 5-aminoallylU, or combinations thereof. In certain embodiments, at least one of the modifications in the combination is an "end" modification such as terminal phosphate, a PEG, a terminal amine, a terminal linker such as a hydrocarbon linker, a substituted hydrocarbon linker, a squarate linker, a triazolo linker, an internal linker such as 2-(4-butylamidofluorescein)propane-1,3-diol bis(phosphodiester) linker, a linker conjugated to a dye, a linker conjugated to a non-fluorescent label, a linker conjugated to a tag or a linker conjugated to a solid support such as for example a bead or microarray. In certain embodiments, at least two of the modifications in the combination comprise a 2'-O-methyl nucleotide and phosphorothioate internucleotide linkage, a 2'-O-methyl nucleotide and phosphonoacetate internucleotide linkage, or a 2'-O-methyl nucleotide and thiophosphonoacetate internucleotide linkage. In certain embodiments, at least two of the modifications in the combination comprise a 2'-O-methyl nucleotide and phosphonocarboxylate internucleotide linkage, a 2'-O-methyl nucleotide and phosphonocarboxylate ester internucleotide linkage, a 2'-O-methyl nucleotide and thiophosphonocarboxylate internucleotide linkage, a 2'-O-methyl nucleotide and thiophosphonocarboxylate ester internucleotide linkage, or combinations thereof. In other embodiments, the modifications in the combination further comprise a 2-thiouracil, 2-thiocytosine, 4-thiouracil, 6-thioguanine, 2-aminoadenine, 2-aminopurine, pseudouracil, inosine, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-methylcytosine, 5-methyluracil, 5-hydroxymethylcytosine, 5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil, 5-allyluracil, 5-allylcytosine, 5-aminoallyluracil, 5-aminoallyl-cytosine, or an abasic nucleotide.

In certain embodiments, at least one of the modifications in the combination comprises a 2'-O-methyl-3'-phosphorothioate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-O-methyl-3'-phosphonoacetate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-O-methyl-3'-thiophosphonoacetate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-halo-3'-phosphorothioate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-halo-3'-phosphonoacetate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-halo-3'-thiophosphonoacetate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-fluoro-3'-phosphorothioate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-fluoro-3'-phosphonoacetate. In certain embodiments, at least one of the modifications in the combination comprises a 2'-fluoro-3'-thiophosphonoacetate. Possible combinations of at least two or three modifications are represented in FIG. **6** and FIG. **7** respectively and are incorporated herein by reference.

In certain embodiments, the guide RNA comprises an oligonucleotide represented by Formula (III) or Formula (IV):

$$W—Y-Q \quad \text{(III); or}$$

$$Y—W—X-Q \quad \text{(IV)}$$

wherein Q and W each independently represent a nucleotide or a stretch of nucleotides of the oligonucleotide comprising at least one modification and Y and X each independently represent an unmodified portion of the oligonucleotide.

In certain embodiments, W is within the 5' portion of the guide RNA. In certain embodiments, W is at least partially within the first five (5) nucleotides of the 5' portion of the guide RNA. In certain embodiments, W is at least partially within the first three (3) nucleotides of the 5' portion of the guide RNA. In certain embodiments, W is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA.

In certain embodiments, Q is within the 3' portion of the guide RNA. In certain embodiments, Q is at least partially within the last five (5) nucleotides of the 3' portion of the guide RNA. In certain embodiments, Q is at least partially within the last three (3) nucleotides of the 3' portion of the guide RNA. In certain embodiments, Q is within the internal region (i.e., between the 5' end and the 3' end) of the guide RNA.

In certain embodiments, W comprises an end modification as described above, such as a 5' end or a 3' end modification. In certain embodiments, the end modification comprises dimethoxytrityl.

In certain embodiments, at least one of W or Q comprises a modified base as described above. In certain embodiments, at least one of W or Q comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 modified bases. In certain embodiments, at least one of W or Q comprises more than one modified base, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 modified bases.

In certain embodiments, at least one of W or Q comprises a modified sugar as described above. In certain embodiments, at least one of W or Q comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 modified sugars. In certain embodiments, at least one of W or Q comprises more than one, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 modified sugars.

In certain embodiments, at least one of W or Q comprises a modified backbone (i.e., an internucleotide linkage other than a phosphodiester) as described above. In certain embodiments, at least one of W or Q comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 modified internucleotide linkages. In certain embodiments, at least one of W or Q comprises more than one, such as 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 modified internucleotide linkages.

In certain embodiments, at least one of W or Q comprises a 2'-O-methyl nucleotide, a 2'-F nucleotide, a 2'-amino nucleotide, a 2'-deoxy nucleotide, a 2-thiouridine nucleotide, a 2-aminoadeosine nucleotide, a 6-thioguanosine nucleotide, a 5-methylcytidine nucleotide, a 5-aminoallyluridine nucleotide, a Z nucleotide, a 3'-phosphorothioate internucleotide linkage, a 3'-phosphorothioate internucleotide linkage, a 3'-phosphonoacetate internucleotide linkage, a 3'-phosphonoacetate ester internucleotide linkage, a 3'-thiophosphonoacetate internucleotide linkage, a 3'-thiophosphonoacetate ester internucleotide linkage, a 3'-methylphosphonate internucleotide linkage, a 3'-boranophosphonate internucleotide linkage, a 3'-phosphorodithioate internucleotide linkage, or combinations thereof.

In certain embodiments, at least one of W or Q comprises a 2'-O-methyl and a 3'-phosphorothioate group on the same nucleotide. In certain embodiments, at least one of W or Q comprises a 2'-O-methyl and a 3'-phosphonoacetate group linkage on the same nucleotide. In certain embodiments, at least one of W or Q comprises a 2'-O-methyl and 3'-thiophosphonoacetate group on the same nucleotide. In certain embodiments, at least one of W or Q comprises a 2'-F and a 3'-phosphorothioate group on the same nucleotide. In certain embodiments, at least one of W or Q comprises a 2'-F and a 3'-phosphonoacetate group linkage on the same nucleotide. In certain embodiments, at least one of W or Q comprises a 2'-F and 3'-thiophosphonoacetate group on the same nucleotide.

In certain embodiments, at least one of W or Q comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 modified nucleotides. In certain embodiments, each of the modified nucleotides within at least one of W or Q comprises the same modification or modifications. In certain embodiments, W comprises a modified nucleotide that is different than a modified nucleotide in Q. In certain embodiments, at least one of W or Q comprises two or more modified nucleotides. In certain embodiments, at least one of W or Q comprises three or more modified nucleotides. In certain embodiments, the modified nucleotides are not arranged contiguously in the sequence, or at least not entirely, as one or more unmodified nucleotides may intercede. In certain embodiments, the modified nucleotides are arranged contiguously. In certain embodiments, at least one of W or Q comprises at least one contiguous stretch of modified nucleotides. In certain embodiments, at least one of W or Q comprises a contiguous stretch of at least three (3) modified nucleotides. In certain embodiments, at least one of W or Q comprises a contiguous stretch of at least four (4) modified nucleotides. In certain embodiments, at least one of W or Q comprises a contiguous stretch of at least five (5) modified nucleotides.

In certain embodiments, the guide RNA comprises a nucleotide sequence of Formula (V) or Formula (VI):

$$M_mN_nM'_{m'}N'_{n'}, \quad \text{(Formula V); or}$$

$$M_mN_nM'_{m'}N'_{n'}M''_{m''} \quad \text{(Formula VI)}$$

wherein each M independently represents a modified ribonucleotide;

wherein each N independently represents an unmodified ribonucleotide;

wherein each M' independently represents a modified ribonucleotide;

wherein each N' independently represents an unmodified ribonucleotide;

wherein each M" independently represents a modified ribonucleotide;

wherein m is an integer between 0 and 40, n is an integer between 0 and 130, m' is an integer between 0 and 10, n' is an integer between 0 and 130, m" is an integer between 0 and 10, provided that m+m'+m" is greater than or equal to 1 and $50<m+n+m'+n'+m''\leq 150$.

In certain embodiments, each M is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, and a 2'-deoxynucleotide. In certain embodiments, each M is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, and a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M is independently selected from the group consisting of a 2'-O-methyl-3'-PACE ribonucleotide and a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, where m>1, any given M is the same or different from any other M. In certain embodiments, where m>1, each M comprises the same modification or modifications.

In certain embodiments, each M' is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, and a 2'-deoxynucleotide. In certain embodiments, each M' is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, and a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M' is independently selected from the group consisting of a 2'-O-methyl-3'-PACE ribonucleotide and a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, where m'>1, any given M' is the same or different from any other M'. In certain embodiments, where m'>1, each M' comprises the same modification or modifications.

In certain embodiments, each M" is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, and a 2'-deoxynucleotide. In certain embodiments, each M" is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, and a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M" is independently selected from the group consisting of a 2'-O-methyl-3'-PACE ribonucleotide and a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, where m">1, any given M" is the same or different from any other M". In certain embodiments, where m'>1, each M" comprises the same modification or modifications.

In certain embodiments, each M is a 2'-O-methyl-3'-PACE ribonucleotide; m is selected from an integer between 1 and 10; each N is independently selected from the group consisting of A, U, C, and G; n is selected from an integer between 10 and 130; each M' is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S)ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, a 2'-deoxynucleotide, and a Z nucleotide; m' is selected from an integer between 1 and 10; each N is independently selected from the group consisting of A, U, C, and G; and n' is selected from an integer between 0 and 130. In certain embodiments, each M' is a 2'-O-methyl-3'-PACE ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl-3'-P(S) ribonucleotide. In certain embodiments, each M' is a Z nucleotide.

In certain embodiments, each M is a 2'-O-methyl-3'-thioPACE ribonucleotide; m is selected from an integer between 1 and 10; each N is independently selected from the group consisting of A, U, C, and G; n is selected from an integer between 10 and 130; each M' is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, a 2'-deoxynucleotide, and a Z nucleotide; m' is selected from an integer between 1 and 10; each N is

independently selected from the group consisting of A, U, C, and G; and n' is selected from an integer between 0 and 130. In certain embodiments, each M' is a 2'-O-methyl-3'-PACE ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl-3'-P(S) ribonucleotide. In certain embodiments, each M' is a Z nucleotide.

In certain embodiments, each M is a 2'-O-methyl-3'-P(S) ribonucleotide; m is selected from an integer between 1 and 10; each N is independently selected from the group consisting of A, U, C, and G; n is selected from an integer between 10 and 130; each M' is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, a 2'-deoxynucleotide, and a Z nucleotide; m' is selected from an integer between 1 and 10; each N is independently selected from the group consisting of A, U, C, and G; and n' is selected from an integer between 0 and 130. In certain embodiments, each M' is a 2'-O-methyl-3'-PACE ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl ribonucleotide. In certain embodiments, each M' is a 2'-O-methyl-3'-P(S)ribonucleotide. In certain embodiments, each M' is a Z nucleotide.

In certain embodiments, each M is independently selected from the group consisting of a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, a 2'-deoxynucleotide, and a Z nucleotide; m is selected from an integer between 0 and 10; each N is independently selected from the group consisting of A, U, C, and G; n is selected from an integer between 10 and 15; each M' is a 2'-O-methyl ribonucleotide; m' is selected from an integer between 1 and 5; each N is independently selected from the group consisting of A, U, C, and G; and n' is selected from an integer between 0 and 130. In certain embodiments, each M is a 2'-O-methyl-3'-PACE ribonucleotide. In certain embodiments, each M is a 2'-O-methyl-3'-thioPACE ribonucleotide. In certain embodiments, each M is a 2'-O-methyl ribonucleotide. In certain embodiments, each M is a 2'-O-methyl-3'-P(S)ribonucleotide. In certain embodiments, m is 0; n is selected from an integer between 10 and 15, m' is selected from an integer between 1 and 5; and n' is selected from an integer between 0 and 130.

In certain embodiments, at least one of the modifications in the combination is a stability-altering modification. In certain embodiments, at least one of the modifications in the combination increases nuclease resistance of the guide RNA relative to a guide RNA without the modification, thus it enhances the stability of the guide RNA.

In certain embodiments, at least one of the modifications in the combination is a stability-enhancing modification as described above.

In certain embodiments, at least one of the modifications in the combination is a specificity-altering modification as described above.

In certain embodiments, at least one of the modifications in the combination alters RNA base pairing. In certain embodiments, at least one of the modifications in the combination lowers the Tm of a base pairing interaction as described above. In certain embodiments, at least one of the modifications in the combination raises the Tm of a base pairing interaction as described above.

In certain embodiments, at least one of the modifications in the combination alters transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, at least one of the modifications in the combination increases transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, at least one of the modifications in the combination decreases transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, at least one of the transfection-increasing modifications in the combination comprises a phosphonoacetate alkyl ester internucleotide linkage, such as a phosphonoacetate methyl ester internucleotide linkage.

In certain embodiments, at least one of the modifications in the combination enhances stability and specificity of the guide RNA relative to a guide RNA without the modification. In certain embodiments, at least one of the modifications in the combination enhances stability and transfection efficiency of the guide RNA relative to a guide RNA without the modification. In certain embodiments, at least one of the modifications in the combination enhances specificity and transfection efficiency of the guide RNA relative to a guide RNA without the modification.

In certain embodiments, at least one of the modifications in the combination alters the secondary structure of the guide RNA. This modification alters the base-pairing of any of the RNA/RNA internal duplexes in the guide RNA. Some of these modifications increase the base pairing of the RNA/RNA structure or alternatively increase the Tm of the RNA/RNA duplex, whereas other modifications decrease the base pairing (or Tm) of the RNA/RNA duplex or duplexes. Such modifications include base modified nucleotides, particularly UNA nucleotides such as the 2-thiouridine and 2-aminoadenosine pair, the Z/P nucleotide pair, the isoC/isoG pair, the 6-thioG/5-methylpyrimidine pair, and nucleotides with modifications on the sugar or the internucleotide linkages as discussed before.

In certain embodiments, the combination includes at least one modification or a set of modifications that increases nucleases resistance (i.e., stability) with at least one modification or a set of modifications that increases specificity (i.e., reduces off-target effects). In certain embodiments, the combination includes at least one modification or a set of modifications that increases nucleases resistance (i.e., stability) with at least one modification or a set of modifications that raises the Tm of some bases pairing in the guide RNA. In certain embodiments, the combination includes at least one modification or a set of modifications that increases nucleases resistance (i.e., stability) with at least one modification or a set of modifications that lowers the Tm of some bases pairing of the guide RNA. In certain embodiments, the combination includes at least one modification or a set of modifications that increases nuclease resistance (i.e., stability), at least one modification or a set of modifications that increases the Tm of some bases paring in the guide RNA, and at least one modification or a set of modifications that decreases the Tm of some base paring elsewhere in the guide RNA. In certain embodiments, the combination includes at least one modification or a set of modifications that increases nuclease resistance (i.e., stability) and at least one modification or a set of modifications that increases the binding of the guide RNA to Cas protein. In certain embodiments, the combination includes at least one modification or a set of modifications that increases nuclease resistance (i.e., stability) and at least one modification or a set of modifications that decreases the binding of the guide RNA to Cas protein.

In certain embodiments, the guide RNA comprises a combination of the different types of modifications.

D. Guide RNA Structure

In certain embodiments, the guide RNA is able to form a complex with a CRISPR-associated-protein. In certain embodiments, the CRISPR-associated protein is provided by or is derived from a CRISPR-Cas type II system, which has an RNA-guided polynucleotide binding and/or nuclease activity. In certain embodiments, the CRISPR-associated protein is Cas9, a Cas9 mutant, or a Cas9 variant. In certain embodiments, the CRISPR-associated protein is the Cas9 nuclease from *Streptococcus pyogenes*. In certain embodiments, the CRISPR-associated protein is the Cas9 nuclease from *Streptococcus thermophilus*. In certain embodiments, the CRISPR-associated protein is the Cas9 nuclease from *Staphylococcus aureus*. In certain embodiments, the synthetic guide RNA or a synthetic guide RNA:CRISPR-associated protein complex maintains functionality of natural guide RNA or a complex that does not have modified nucleotides. In certain embodiments, the functionality includes binding a target polynucleotide. In certain embodiments, the functionality includes nicking a target polynucleotide. In certain embodiments, the functionality includes cleaving a target polynucleotide. In certain embodiments, the target polynucleotide is within a nucleic acid in vitro. In certain embodiments, the target polynucleotide is within the genome of a cell in vivo or in vitro (such as in cultured cells or cells isolated from an organism). In certain embodiments, the target polynucleotide is a protospacer in DNA.

In certain embodiments, the crRNA segment comprises from 25 to 80 nucleotides. In certain embodiments, the crRNA segment comprises a guide sequence that is capable of hybridizing to a target sequence. In certain embodiments, the guide sequence is complementary to the target sequence or a portion thereof. In certain embodiments, the guide sequence comprises from 15 to 30 nucleotides. In certain embodiments, the crRNA segment comprises a stem sequence. In certain embodiments, the stem sequence comprises from 10 to 50 nucleotides. In certain embodiments, the crRNA segment comprises a 5'-overhang sequence. In certain embodiments, the 5'-overhang sequence comprises from 1 to 10 nucleotides, alternatively 1 to 5 nucleotides, alternatively 1, 2 or 3 nucleotides. In certain embodiments, the crRNA comprises both (i) a guide sequence that is capable of hybridizing to a target sequence and (ii) a stem sequence. In certain embodiments, the crRNA comprises (i) a 5'-overhang sequence, (ii) a guide sequence that is capable of hybridizing to a target sequence, and (iii) a stem sequence. In certain embodiments wherein the crRNA segment comprises a stem sequence, the tracrRNA segment comprises a nucleotide sequence that is partially or completely complementary to the stem sequence of the crRNA segment. In certain embodiments, the tracrRNA segment comprises at least one more duplex structure.

In certain embodiments, the guide RNA is a single guide RNA. In certain embodiments, the guide RNA is a single guide RNA, wherein the crRNA segment and the tracrRNA segment are linked through a loop L. In certain embodiments, the loop L comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides. In certain embodiments, the loop L comprises a nucleotide sequence of GNRA, wherein N represents A, C, G, or U and R represents A or G. In certain embodiments, the loop L comprises a nucleotide sequence of GAAA. In certain embodiments, the guide RNA comprises more than one loop.

The guide RNA comprises a 5' portion (i.e., the 5' half) and a 3' portion (i.e., the 3' half). In certain embodiments, the crRNA segment is 5' (i.e., upstream) of the tracrRNA segment. In certain embodiments, the tracrRNA segment is 5' relative to the crRNA segment.

In certain embodiments, the guide RNA comprises at least two separate RNA strands, for example, a crRNA strand and a separate tracrRNA strand. See, for example, FIG. **5**A. In certain embodiments, each of the strands is a synthetic strand comprising one or more modifications. In certain embodiments, at least one of the strands is a synthetic strand comprising one or more modifications. In certain embodiments, the strands function together to guide binding, nicking, or cleaving of a target polynucleotide by a Cas protein, such as Cas9. In certain embodiments, the crRNA sequence and the tracrRNA sequence are on separate stands and hybridize to each other via two complementary sequences to form a stem or duplex.

In certain embodiments, the guide RNA is a single guide RNA comprising a crRNA sequence and a tracrRNA sequence. See, for example, FIG. **5**B. In certain embodiments, the crRNA sequence and the tracrRNA sequence are connected by a loop sequence or "loop." In certain embodiments, a single guide RNA comprises a 5' portion and a 3' portion, wherein the crRNA sequence is upstream of the tracrRNA sequence.

In certain embodiments, the total length of the two RNA pieces can be about 50-220 (e.g., about 55-200, 60-190, 60-180, 60-170, 60-160, 60-150, 60-140, 60-130, and 60-120) nucleotides in length, such as about 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or 220 nucleotides in length. Similarly, the single guide RNA (e.g., FIG. **5**B) can be about 50-220 (e.g., about 55-200, 60-190, 60-180, 60-170, 60-160, 60-150, 60-140, 60-130, and 60-120) nucleotides in length, such as about 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or 220 nucleotides in length.

As shown in FIGS. **5**A and **5**B, the synthetic guide RNA comprises (i) a crRNA sequence that comprises (a) a guide sequence (e.g., segment G_1-G_n, where each G represents a nucleotide in the guide sequence) capable of hybridizing to a target sequence in a nucleic acid, (b) a first stem sequence (e.g., segment X_1-X_n, where each X represents a nucleotide in the first stem sequence) capable of hybridizing partially or completely to a second stem sequence, and, optionally (c) a 5'-overhang sequence (e.g., segment O_1-O_n, where each 0 represents a nucleotide in the overhang sequence), and (ii) a tracrRNA sequence that comprises the second stem sequence (e.g., segment Y_1-Y_n, where each Y represents a nucleotide in the second stem sequence). The tracrRNA sequence further comprises segment T_1-T_n, where each T represents a nucleotide in the tracrRNA sequence. The synthetic guide RNA shown in FIG. **5**A includes one or more modifications. Likewise, the synthetic guide RNA shown in FIG. **5**B includes one or more modifications. In certain embodiments, the modification is located at any point along the length of the crRNA, the tracrRNA, or the single guide RNA comprising a crRNA segment, a tracrRNA segment, and, optionally, a loop. In certain embodiments, any nucleotide represented by O, G, X, Y, or T in the synthetic guide RNA shown in FIGS. **5**A and **5**B may be a modified nucleotide. The guide RNA shown in FIG. **5**B represents a single guide RNA (sgRNA) where the crRNA segment and the tracrRNA segment are connected by a loop having the sequence GNRA, wherein N represents A, C, G, or U, and R represents A or G.

In certain embodiments, the crRNA segment of the guide RNA is 25-70 (e.g., 30-60, 35-50, or 40-45) nucleotides in length. In certain embodiments, the guide sequence is 12-30 (e.g., 16-25, 17-20, or 15-18) nucleotides in length. In some embodiments, a 5' portion of the crRNA does not hybridize or only partially hybridizes with the target sequence. For example, there can be a 5'-overhang on the crRNA segment.

In certain embodiments, the single guide RNA comprises a central portion including the stem sequence of the crRNA segment, the stem sequence of the tracrRNA segment, and, optionally, a loop that covalently connects the crRNA segment to the tracrRNA segment. In certain embodiments, the central segment of the single guide RNA is 8-60 (e.g., 10-55, 10-50, or 20-40) nucleotides in length.

In certain embodiments, the tracrRNA segment of the guide RNA is 10-130 (e.g., 10-125, 10-100, 10-75, 10-50, or 10-25) nucleotides in length. In certain embodiments, the tracrRNA segment includes one or more hairpin or duplex structures in addition to any hairpin or duplex structure in the central segment.

In certain embodiments, the tracrRNA is truncated compared to a reference tracrRNA, such as a naturally existing mature tracrRNA. A range of lengths has been shown to function in both the separate type (FIG. **5**A) and the chimeric sgRNA type (FIG. **5**B). For example, in certain embodiments, tracrRNA may be truncated from its 3' end by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35 or 40 nts. In certain embodiments, the tracrRNA molecule may be truncated from its 5' end by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75 or 80 nts. In certain embodiments, the tracrRNA molecule may be truncated from both the 5' and 3' end, e.g., by at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15 or 20 nts from the 5' end and at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35 or 40 nts from the 3' end. See, e.g., Jinek et al. (2012) *Science,* 337, 816-21; Mali et al. (2013) *Science,* 339:6121, 823-6; Cong et al. (2013) *Science,* 339:6121, 819-23; and Hwang et al. (2013) *Nat. Biotechnol.* 31:3, 227-9; Jinek et al. (2013) *eLife,* 2, e00471. In certain embodiments, the tracrRNA is untruncated.

In certain embodiments, the disclosed modifications are in the crRNA segment or the tracrRNA segment or both. In certain embodiments, the disclosed modifications are in the guide sequence of the crRNA segment. In certain embodiments, the disclosed modifications are in the stem sequence of the crRNA segment. In certain embodiments, the disclosed modifications are in the 5'-overhang sequence of the crRNA segment. In certain embodiments, the disclosed modifications are in the stem sequence of the tracrRNA segment. In certain embodiments, the disclosed modifications are in the loop sequence of the guide RNA. In certain embodiments, the disclosed modifications are in the 5' portion of the guide RNA. In certain embodiments, the disclosed modifications are in the 3' portion of the guide RNA. In certain embodiments, the disclosed modifications are in the 5' portion of the guide RNA and the 3' portion of the guide RNA.

E. Synthesis of Guide RNA

In certain embodiments, guide RNAs, including single guide RNAs (sgRNAs; see FIGS. **1** and **5**B) are produced by chemical synthesis using the art of synthetic organic chemistry. A guide RNA that comprises any nucleotide other than the four predominant ribonucleotides, namely A, C, G, and U, whether unnatural or natural, such as a pseudouridine, inosine or a deoxynucleotide, possesses a chemical modification or substitution at the nucleotide which is chemically/structurally distinct from any of the four predominant nucleotides in RNAs.

The synthetic guide RNAs described herein can be chemically synthesized. For example, the synthetic guide RNAs can be synthesized using TC chemistry by the method described in Dellinger et al. (2011) *J. Am. Chem. Soc.,* 133, 11540, U.S. Pat. No. 8,202,983, and US Patent Application 2010/0076183A1, the contents of which are incorporated by reference in their entireties. "TC chemistry" refers to the composition and methods of using RNA monomeric nucleotide precursors protected on the 2'-hydroxyl moiety by a thionocarbamate protecting group, to synthesize unmodified RNA or modified RNA comprising one or more modified nucleotides. The ability to chemically synthesize relatively long RNAs (as long as 200 mers or more) using TC-RNA chemistry allows one to produce guide RNAs with special features capable of outperforming those enabled by the four predominant ribonucleotides (A, C, G and U). Some synthetic guide RNAs described herein can also be made using methods known in the art that include in vitro transcription and cell-based expression. For example, 2'-fluoro NTPs can be incorporated into synthetic guide RNAs produced by cell-based expression.

Synthesis of guide RNAs can also be accomplished by chemical or enzymatic synthesis of RNA sequences that are subsequently ligated together by enzymes, or chemically ligated by chemical ligation, including but not limited to cyanogen bromide chemistry, "click" chemistry as published by R. Kumar et al. (2007) *J. Am. Chem. Soc.,* 129, 6859-64, or squarate conjugation chemistry as described by K. Hill in WO2013176844 titled "Compositions and methods for conjugating oligonucleotides."

As further described below, a guide RNA disclosed herein, including those comprising modified nucleotides and/or modified internucleotide linkages, can be used to perform various CRISPR-mediated functions (including but not limited to editing genes, regulating gene expression, cleaving target sequences, and binding to target sequences) in vitro or in vivo, such as in cell-free assays, in intact cells, or in whole organisms. For in vitro or in vivo applications, the RNA can be delivered into cells or whole organisms in any manner known in the art.

Libraries and Arrays

In one aspect, the present invention provides a set or library of multiple guide RNAs. In certain embodiments, the library contains two or more guide RNAs disclosed herein. The library can contain from about 10 to about 10^7 individual members, e.g., about 10 to about 10^2, about 10^2 to about 10^3, about 10^3 to about 10^5, from about 10^5 to about 10^7 members. An individual member of the library differs from other members of the library at least in the guide sequence, i.e., the DNA targeting segment of the gRNA. On the other hand, in certain embodiments, each individual member of a library can contain the same or substantially the same nucleotide sequence for the tracrRNA segment as all the other members of the library. In this way, the library can comprise members that target different polynucleotides or different sequences in one or more polynucleotides.

In certain embodiments, the library comprises at least 10^2 unique guide sequences. In certain embodiments, the library comprises at least 10^3 unique guide sequences. In certain embodiments, the library comprises at least 10^4 unique guide sequences. In certain embodiments, the library comprises at least 10^5 unique guide sequences. In certain embodiments, the library comprises at least 10^6 unique guide sequences. In certain embodiments, the library com-

prises at least 10^7 unique guide sequences. In certain embodiments, the library targets at least 10 different polynucleotides. In certain embodiments, the library targets at least 10^2 different polynucleotides. In certain embodiments, the library targets at least 10^3 different polynucleotides. In certain embodiments, the library targets at least 10^4 different polynucleotides. In certain embodiments, the library targets at least 10^5 different polynucleotides. In certain embodiments, the library targets at least 10^6 different polynucleotides. In certain embodiments, the library targets at least 10^7 different polynucleotides.

In certain embodiments, the library comprises a collection of guide RNAs having the same sequence and the same modifications in a progressively shifted window that moves across the sequence of the members in the library. In certain embodiments, the windows collectively cover the entire length of the RNA.

In certain embodiments, the library allows one to conduct high-throughput, multi-target genomic manipulations and analyses. In certain embodiments, only the DNA-targeting segments of the guide RNAs are varied, while the Cas protein-binding segment is the same. In certain embodiments, a first portion of the library comprises guide RNAs possessing a Cas-binding segment that recognizes, binds and directs a particular Cas protein and a second portion of the library comprises a different Cas-binding segment that recognizes, binds and directs a different Cas protein (e.g., a Cas protein from a different species), thereby allowing the library to function with two or more orthogonal Cas proteins. In certain embodiments, induced expression of a first orthogonal Cas protein utilizes the portion of the library which interacts with the first orthogonal Cas protein. In certain embodiments, induced expression of a first and second orthogonal Cas protein utilizes the portions of the library which interact with the first and second orthogonal Cas proteins, respectively. In certain embodiments, induced expression of the first and second orthogonal Cas proteins occur at different times. Accordingly, one can carry out large-scale gene editing or gene regulation by specifically manipulating or modifying multiple targets as specified in the library.

In certain embodiments, the library is an "arrayed" library, namely a collection of different features or pools of features in an addressable arrangement. For example, features of an array can be selectively cleaved and transferred to a microtiter plate such that each well in the plate contains a known feature or a known pool of features. In some other embodiments, the library is synthesized in a 48-columns or in a 96-columns microtiter plate format or in a 384-columns plate.

In certain embodiments, synthesis of the guide RNA of this invention may be conducted on a solid support having a surface to which chemical entities may bind. In some embodiments, guide RNAs being synthesized are attached, directly or indirectly, to the same solid support and may form part of an array. An "array" is a collection of separate molecules of known monomeric sequence each arranged in a spatially defined and a physically addressable manner, such that the location of each sequence is known. An "array," or "microarray" used interchangeably herein includes any one-dimensional, two-dimensional or substantially two-dimensional (as well as a three-dimensional) arrangement of addressable regions bearing a particular chemical moiety or moieties (such as ligands, e.g., biopolymers such as polynucleotide or oligonucleotide sequences (nucleic acids), polypeptides (e.g., proteins), carbohydrates, lipids, etc.) associated with that region. An array is "addressable" when it has multiple regions of different moieties (e.g., different polynucleotide sequences) such that a region (i.e., a "feature" of the array) at a particular predetermined location (i.e., an "address") on the array will detect a particular target or class of targets (although a feature may incidentally detect non-targets of that feature). Array features are typically, but need not be, separated by intervening spaces. The number of features that can be contained on an array will largely be determined by the surface area of the substrate, the size of a feature and the spacing between features. Arrays can have densities of up to several hundred thousand or more features per cm^2, such as 2,500 to 200,000 features/cm^2. The features may or may not be covalently bonded to the substrate.

Suitable solid supports may have a variety of forms and compositions and derive from naturally occurring materials, naturally occurring materials that have been synthetically modified, or synthetic materials. Examples of suitable support materials include, but are not limited to, silicas, silicon and silicon oxides, teflons, glasses, polysaccharides such as agarose (e.g., Sepharose® from Pharmacia) and dextran (e.g., Sephadex® and Sephacyl®, also from Pharmacia), polyacrylamides, polystyrenes, polyvinyl alcohols, copolymers of hydroxyethyl methacrylate and methyl methacrylate, and the like. In some embodiments, the solid support is a plurality of beads.

The initial monomer of the guide RNAs to be synthesized on the substrate surface can be bound to a linker which in turn is bound to a surface hydrophilic group, e.g., a surface hydroxyl moiety present on a silica substrate. In some embodiments, a universal linker is used. In some other embodiments, the initial monomer is reacted directly with, e.g., a surface hydroxyl moiety. Alternatively, guide RNAs can be synthesized first according to the present invention, and attached to a solid substrate post-synthesis by any method known in the art. Thus, the present invention can be used to prepare arrays of guide RNAs wherein the oligonucleotides are either synthesized on the array, or attached to the array substrate post-synthesis. Subsequently, the guide RNAs or a pool or a plurality of pools of guide RNAs can optionally and selectively be cleaved from the array substrate and be used as a library or libraries.

IV. Cas Proteins

As mentioned above, a functional CRISPR-Cas system also requires a protein component (e.g., a Cas protein, which may be a Cas nuclease) that provides a desired activity, such as target binding or target nicking/cleaving. In certain embodiments, the desired activity is target binding. In certain embodiments, the desired activity is target nicking or target cleaving. In certain embodiments, the desired activity also includes a function provided by a polypeptide that is covalently fused to a Cas protein, as disclosed herein. In certain embodiments, the desired activity also includes a function provided by a polypeptide that is covalently fused to a nuclease-deficient Cas protein, as disclosed herein. Examples of such a desired activity include a transcription regulation activity (either activation or repression), an epigenetic modification activity, or a target visualization/identification activity, as described below. The Cas protein can be introduced into an in vitro or in vivo system as a purified or non-purified (i) Cas protein or (ii) mRNA encoded for expression of the Cas protein or (iii) linear or circular DNA encoded for expression of the protein. Any of these 3 methods of providing the Cas protein are well known in the art and are implied interchangeably when mention is made

herein of a Cas protein or use of a Cas protein. In certain embodiments, the Cas protein is constitutively expressed from mRNA or DNA. In certain embodiments, the expression of Cas protein from mRNA or DNA is inducible or induced.

In certain embodiments, the Cas protein is chemically synthesized (see e.g., Creighton, "Proteins: Structures and Molecular Principles," W.H. Freeman & Co., NY, 1983), or produced by recombinant DNA technology as described herein. For additional guidance, skilled artisans may consult Frederick M. Ausubel et al., "Current Protocols in Molecular Biology," John Wiley & Sons, 2003; and Sambrook et al., "Molecular Cloning, A Laboratory Manual," Cold Spring Harbor Press, Cold Spring Harbor, N.Y., 2001).

In certain embodiments, the Cas protein is provided in purified or isolated form. In certain embodiments, the Cas protein is provided at about 80%, about 90%, about 95%, or about 99% purity. In certain embodiments, the Cas protein is provided as part of a composition. In certain embodiments, the Cas protein is provided in aqueous compositions suitable for use as, or inclusion in, a composition for an RNA-guided nuclease reaction. Those of skill in the art are well aware of the various substances that can be included in such nuclease reaction compositions.

In certain embodiments, a Cas protein is provided as a recombinant polypeptide. In certain examples, the recombinant polypeptide is prepared as a fusion protein. For example, in certain embodiments, a nucleic acid encoding the Cas protein is linked to another nucleic acid encoding a fusion partner, e.g., glutathione-s-transferase (GST), 6×-His epitope tag, or M13 Gene 3 protein. Suitable host cells can be used to expresses the fusion protein. In certain embodiments, the fusion protein is isolated by methods known in the art. In certain embodiments, the fusion protein can be further treated, e.g., by enzymatic digestion, to remove the fusion partner and obtain the Cas protein. Alternatively, Cas protein:guide RNA complexes can be made with recombinant technology using a host cell system or an in vitro translation-transcription system known in the art. Details of such systems and technology can be found in e.g., WO2014144761 WO2014144592, WO2013176772, US20140273226, and US20140273233, the contents of which are incorporated herein by reference in their entireties.

Wild Type Cas Proteins

In certain embodiments, a Cas protein comprises a protein derived from a CRISPR-Cas type I, type II, or type III system, which has an RNA-guided polynucleotide binding and/or nuclease activity. Non-limiting examples of suitable Cas proteins include Cas3, Cas4, Cas5, Cas5e (or CasD), Cash, Cas6e, Cas6f, Cas7, Cas8a1, Cas8a2, Cas8b, Cas8c, Cas9, Cas10, Cas10d, CasF, CasG, CasH, Csy1, Csy2, Csy3, Cse1 (or CasA), Cse2 (or CasB), Cse3 (or CasE), Cse4 (or CasC), Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csz1, Csx15, Csf1, Csf2, Csf3, Csf4, and Cu1966. See e.g., WO2014144761 WO2014144592, WO2013176772, US20140273226, and US20140273233, the contents of which are incorporated herein by reference in their entireties.

In certain embodiments, the Cas protein is derived from a type II CRISPR-Cas system. In certain embodiments, the Cas protein is or is derived from a Cas9 protein. In certain embodiments, the Cas protein is or is derived from a bacterial Cas9 protein, including those identified in WO2014144761. In certain embodiments, the Cas protein is or is derived from a *Streptococcus* sp. or *Staphylococcus* sp. Cas9 protein. In certain embodiments, the Cas protein is or is derived from the *Streptococcus thermophilus* Cas9 protein. In certain embodiments, the Cas protein is or is derived from a the *Streptococcus pyogenes* Cas9 protein. In certain embodiments, the Cas protein is or is derived from the *Staphylococcus aureus* Cas9 protein. In certain embodiments, the Cas protein is or is derived from the *Streptococcus thermophilus* Cas9 protein.

In certain embodiments, the wild type Cas protein is a Cas9 protein. In certain embodiments, the wild type Cas9 protein is the Cas9 protein from *S. pyogenes* (SEQ ID NO: 1). In certain embodiments, the protein or polypeptide can comprise, consist of, or consist essentially of a fragment of SEQ ID NO: 1.

In general, a Cas protein includes at least one RNA binding domain, which interacts with the guide RNA. In certain embodiments, the Cas protein is modified to increase nucleic acid binding affinity and/or specificity, alter an enzymatic activity, and/or change another property of the protein. For example, nuclease (i.e., DNase, RNase) domains of the Cas protein can be modified, mutated, deleted, or inactivated. Alternatively, the Cas protein can be truncated to remove domains that are not essential for the function of the protein. In certain embodiments, the Cas protein is truncated or modified to optimize the activity of the effector domain. In certain embodiments, the Cas protein includes a nuclear localization sequence (NLS) that effects importation of the NLS-tagged Cas protein into the nucleus of a living cell. In certain embodiments, the Cas protein includes two or more modifications.

Mutant Cas Proteins

In some embodiments, the Cas protein can be a mutant of a wild type Cas protein (such as Cas9) or a fragment thereof. In other embodiments, the Cas protein can be derived from a mutant Cas protein. For example, the amino acid sequence of the Cas9 protein can be modified to alter one or more properties (e.g., nuclease activity, binding affinity, stability, etc.) of the protein. Alternatively, domains of the Cas9 protein not involved in RNA-guided cleavage can be eliminated from the protein such that the modified Cas9 protein is smaller than the wild type Cas9 protein. For example, reducing the size of the Cas9 coding sequence can allow it to fit within a transfection vector that otherwise cannot accommodate the wild type sequence, such as the AAV vector among others. In some embodiments, the present system utilizes the Cas9 protein from *S. pyogenes*, either as encoded in bacteria or codon-optimized for expression in eukaryotic cells. Shown below is the amino acid sequence of wild type *S. pyogenes* Cas9 protein sequence (SEQ ID No. 1, Uniprot No. Q99ZW2.

MDKKYSIGL**D**IGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGA

LLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHR

LEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKAD

LRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENP

INASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTP

NFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAI

LLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEI

FFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLR

-continued

KQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPY

YVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDK

NLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVD

LLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKI

IKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQ

LKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDD

SLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKV

MGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHP

VENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDD

SIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNL

TKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI

REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKK

YPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEI

TLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV

QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVE

KGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPK

YSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPE

DNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDK

PIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQ

SITGLYETRIDLSQLGGD

A Cas9 protein generally has at least two nuclease (e.g., DNase) domains. For example, a Cas9 protein can have a RuvC-like nuclease domain and an HNH-like nuclease domain. The RuvC and HNH domains work together to cut both strands in a target site to make a double-stranded break in the target polynucleotide. (Jinek et al., Science, 337: 816-821). In certain embodiments, a mutant Cas9 protein is modified to contain only one functional nuclease domain (either a RuvC-like or an HNH-like nuclease domain). For example, in certain embodiments, the mutant Cas9 protein is modified such that one of the nuclease domains is deleted or mutated such that it is no longer functional (i.e., the nuclease activity is absent). In some embodiments where one of the nuclease domains is inactive, the mutant is able to introduce a nick into a double-stranded polynucleotide (such protein is termed a "nickase") but not able to cleave the double-stranded polynucleotide. For example, an aspartate to alanine (D10A) conversion in a RuvC-like domain converts the Cas9-derived protein into a nickase. Likewise, a histidine to alanine (H840A) conversion in a HNH domain converts the Cas9-derived protein into a nickase. Likewise, an arsparagine to alanine (N863A) conversion in a HNH domain converts the Cas9-derived protein into a nickase.

In certain embodiments, both the RuvC-like nuclease domain and the HNH-like nuclease domain are modified or eliminated such that the mutant Cas9 protein is unable to nick or cleave the target polynucleotide. In certain embodiments, all nuclease domains of the Cas9-derived protein are modified or eliminated such that the Cas9-derived protein lacks all nuclease activity. In certain embodiments, a Cas9 protein that lacks some or all nuclease activity relative to a wild-type counterpart, nevertheless, maintains target recognition activity to a greater or lesser extent.

In any of the above-described embodiments, any or all of the nuclease domains can be inactivated by one or more deletion mutations, insertion mutations, and/or substitution mutations using well-known methods, such as site-directed mutagenesis, PCR-mediated mutagenesis, and total gene synthesis, as well as other methods known in the art.

In certain embodiments, the "Cas mutant" or "Cas variant" is at least 50% (e.g., any number between 50% and 100%, inclusive, e.g., 50%, 60%, 70%, 80%, 90%, 95%, 98%, and 99%) identical to SEQ ID NO: 1. In certain embodiments, the "Cas mutant" or "Cas variant" binds to an RNA molecule (e.g., a sgRNA). In certain embodiments, the "Cas mutant" or "Cas variant" is targeted to a specific polynucleotide sequence via the RNA molecule.

Fusion Proteins

In certain embodiments, the Cas protein is fused to another protein or polypeptide heterologous to the Cas protein to create a fusion protein. In certain embodiments, the heterologous sequence includes one or more effector domains, such as a cleavage domain, a transcriptional activation domain, a transcriptional repressor domain, or an epigenetic modification domain. Additional examples of the effector domain include a nuclear localization signal, cell-penetrating or translocation domain, or a marker domain. In certain embodiments, the effector domain is located at the N-terminal, the C-terminal, or in an internal location of the fusion protein. In certain embodiments, the Cas protein of the fusion protein is or is derived from a Cas9 protein. In certain embodiments, the Cas protein of the fusion protein is or is derived from a modified or mutated Cas protein in which all the nuclease domains have been inactivated or deleted. In certain embodiments, the Cas protein of the fusion protein is or is derived from a modified or mutated Cas protein that lacks nuclease activity. In certain embodiments, the RuvC and/or HNH domains of the Cas protein are modified or mutated such that they no longer possess nuclease activity.

Cleavage Domains

In certain embodiments, the effector domain of the fusion protein is a cleavage domain. As used herein, a "cleavage domain" refers to a domain that cleaves DNA. The cleavage domain can be obtained from any endonuclease or exonuclease. Non-limiting examples of endonucleases from which a cleavage domain can be derived include restriction endonucleases and homing endonucleases. See, for example, New England Biolabs Catalog or Belfort et al. (1997) *Nucleic Acids Res.* 25, 3379-88. Additional enzymes that cleave DNA are known (e.g., 51 Nuclease; mung bean nuclease; pancreatic DNase I; micrococcal nuclease; yeast HO endonuclease). See also Linn et al. (eds.) "Nucleases," Cold Spring Harbor Laboratory Press, 1993. One or more of these enzymes (or functional fragments thereof) can be used as a source of cleavage domains.

In certain embodiments, the cleavage domain can be derived from a type II-S endonuclease. Type II-S endonucleases cleave DNA specifically at sites that are typically several base pairs away from the DNA recognition site of the endonuclease and, as such, have separable recognition and cleavage domains. These enzymes generally are monomers that transiently associate to form dimers to cleave each strand of DNA at staggered locations. Non-limiting examples of suitable type II-S endonucleases include BfiI, BpmI, BsaI, BsgI, BsmBI, BsmI, BspMI, FokI, MboII, and SapI. In certain embodiments, the cleavage domain of the fusion protein is a FokI cleavage domain or a fragment or derivative thereof. See Miller et al. (2007) *Nat. Biotechnol.*

25, 778-85; Szczpek et al. (2007) *Nat. Biotechnol.* 25, 786-93; Doyon et al. (2011) *Nat. Methods,* 8, 74-81.

Transcriptional Activation Domains

In certain embodiments, the effector domain of the fusion protein is a transcriptional activation domain. In general, a transcriptional activation domain interacts with transcriptional control elements and/or transcriptional regulatory proteins (i.e., transcription factors, RNA polymerases, etc.) to increase and/or activate transcription of a gene. In certain embodiments, the transcriptional activation domain is a herpes simplex virus VP16 activation domain, VP64 (which is a tetrameric derivative of VP16), a NFκB p65 activation domain, p53 activation domains 1 and 2, a CREB (cAMP response element binding protein) activation domain, an E2A activation domain, or an NFAT (nuclear factor of activated T-cells) activation domain. In certain embodiments, the transcriptional activation domain is Gal4, Gcn4, MLL, Rtg3, Gln3, Oaf1, Pip2, Pdr1, Pdr3, Pho4, or Leu3. The transcriptional activation domain may be wild type, or it may be a modified or truncated version of the original transcriptional activation domain.

Transcriptional Repressor Domains

In certain embodiments, the effector domain of the fusion protein is a transcriptional repressor domain. In general, a transcriptional repressor domain interacts with transcriptional control elements and/or transcriptional regulatory proteins (i.e., transcription factors, RNA polymerases, etc.) to decrease and/or prohibit transcription of a gene. In certain embodiments, the transcriptional repressor domains is inducible cAMP early repressor (ICER) domains, Kruppel-associated box A (KRAB-A) repressor domains, YY1 glycine rich repressor domains, Sp1-like repressors, E(spI) repressors, IκB repressor, or MeCP2.

Epigenetic Modification Domains

In certain embodiments, the effector domain of the fusion protein is an epigenetic modification domain. In general, epigenetic modification domains alter gene expression by modifying the histone structure and/or chromosomal structure. In certain embodiments, the epigenetic modification domains is a histone acetyltransferase domain, a histone deacetylase domain, a histone methyltransferase domain, a histone demethylase domain, a DNA methyltransferase domain, or a DNA demethylase domain.

Additional Domains

In certain embodiments, the fusion protein further comprises at least one additional domain. Non-limiting examples of suitable additional domains include nuclear localization signals (NLSs), cell-penetrating or translocation domains, and marker domains. An NLS generally comprises a stretch of basic amino acids. See, e.g., Lange et al. (2007) *J. Biol. Chem.,* 282, 5101-5. For example, in certain embodiments, the NLS is a monopartite sequence, such as PKKKRKV (SEQ ID NO: 2) or PKKKRRV (SEQ ID NO: 3). In certain embodiments, the NLS is a bipartite sequence. In certain embodiments, the NLS is KRPAATKKAGQAKKKK (SEQ ID NO: 4).

In certain embodiments, the fusion protein comprises at least one cell-penetrating domain. In certain embodiments, the cell-penetrating domain is a cell-penetrating peptide sequence derived from the HIV-1 TAT protein. As an example, the TAT cell-penetrating sequence can be GRKKRRQRRRPPQPKKKRKV (SEQ ID NO: 5). In certain embodiments, the cell-penetrating domain is TLM (PLSSIFSRIGDPPKKKRKV; SEQ ID NO: 6), a cell-penetrating peptide sequence derived from the human hepatitis B virus. In certain embodiments, the cell-penetrating domain is MPG (GALFLGWLGAAGSTMGAPKKKRKV; SEQ ID NO: 7 or GALFLGFLGAAGSTMGAWSQPKKKRKV; SEQ ID NO: 8). In certain embodiments, the cell-penetrating domain is Pep-1 (KETWWETWWTEWSQPKKKRKV; SEQ ID NO: 9), VP22, a cell penetrating peptide from Herpes simplex virus, or a polyarginine peptide sequence.

In certain embodiments, the fusion protein comprises at least one marker domain. Non-limiting examples of marker domains include fluorescent proteins, purification tags, and epitope tags. In certain embodiments, the marker domain is a fluorescent protein. Non limiting examples of suitable fluorescent proteins include green fluorescent proteins (e.g., GFP, GFP-2, tagGFP, turboGFP, EGFP, Emerald, Azami Green, Monomeric Azami Green, CopGFP, AceGFP, ZsGreen1), yellow fluorescent proteins (e.g. YFP, EYFP, Citrine, Venus, YPet, PhiYFP, ZsYellow1), blue fluorescent proteins (e.g. EBFP, EBFP2, Azurite, mKalama1, GFPuv, Sapphire, T-sapphire), cyan fluorescent proteins (e.g. ECFP, Cerulean, CyPet, AmCyan1, Midoriishi-Cyan), red fluorescent proteins (mKate, mKate2, mPlum, DsRed monomer, mCherry, mRFP1, DsRed-Express, DsRed2, DsRed-Monomer, HcRed-Tandem, HcRedl, AsRed2, eqFP611, mRasberry, mStrawberry, Jred), orange fluorescent proteins (mOrange, mKO, Kusabira-Orange, Monomeric Kusabira-Orange, mTangerine, tdTomato) and any other suitable fluorescent protein. In certain embodiments, the marker domain is a purification tag and/or an epitope tag. Exemplary tags include, but are not limited to, glutathione-S-transferase (GST), chitin binding protein (CBP), maltose binding protein, thioredoxin (TRX), poly(NANP), tandem affinity purification (TAP) tag, myc, AcV5, AU1, AU5, E, ECS, E2, FLAG, HA, nus, Softag 1, Softag 3, Strep, SBP, Glu-Glu, HSV, KT3, S, S1, T7, V5, VSV-G, 6×His, biotin carboxyl carrier protein (BCCP), and calmodulin.

V. Uses and Methods

In one aspect, the present invention provides a method for cleaving a target polynucleotide with a Cas protein. The method comprises contacting the target polynucleotide with (i) a guide RNA or a set of guide RNA molecules described herein, and (ii) a Cas protein. In certain embodiments, the method results in a double-strand break in the target polynucleotide. In certain embodiments, the Cas protein is a Cas protein having a single-strand nicking activity. In certain embodiments, the method results in a single-strand break in the target polynucleotide. In certain embodiments, a complex comprising a guide RNA and Cas protein having a single-strand nicking activity is used for sequence-targeted single-stranded DNA cleavage, i.e., nicking.

In one aspect, the present invention provides a method for cleaving two or more target polynucleotides with a Cas protein. The method comprises contacting the target polynucleotides with (i) a set of guide RNA molecules described herein, and (ii) a Cas protein. In certain embodiments, the method results in double-strand breaks in the target polynucleotides. In certain embodiments, the Cas protein is a Cas protein having a single-strand nicking activity. In certain embodiments, the method results in single-strand breaks in the target polynucleotides. In certain embodiments, a complex comprising a guide RNA and Cas protein having a single-strand nicking activity is used for sequence-targeted single-stranded DNA cleavage, i.e., nicking.

In one aspect, the present invention provides a method for binding a target polynucleotide with a Cas protein. The method comprises contacting the target polynucleotide with (i) a guide RNA or a set of guide RNA molecules described herein and (ii) a Cas protein, to result in binding of the target

polynucleotide with the Cas protein. In certain embodiments, the Cas protein is a Cas variant. In certain embodiments, the Cas variant lacks some or all nuclease activity relative to a counterpart wild-type Cas protein.

In one aspect, the present invention provides a method for binding two or more target polynucleotides with a Cas protein. The method comprises contacting the target polynucleotides with (i) a set of RNA molecules described herein and (ii) a Cas protein, to result in binding of the target polynucleotides with the Cas protein. In certain embodiments, the Cas protein is a Cas variant. In certain embodiments, the Cas variant lacks some or all nuclease activity relative to a counterpart wild-type Cas protein.

In one aspect, the present invention provides a method for targeting a Cas protein to a target polynucleotide. The method comprises contacting the Cas protein with a guide RNA or a set of guide RNA molecules described herein. In certain embodiments, the method results in formation of a guide RNA:Cas protein complex. In certain embodiments, the Cas protein is a wild type Cas9 protein. In certain embodiments, the Cas protein is a mutant or variant of a Cas9 protein. In certain embodiments, the Cas protein is a Cas protein having a single-strand nicking activity. In certain embodiments, the Cas protein is a Cas protein lacking nuclease activity (e.g., a nuclease-deficient mutant of Cas protein). In certain embodiments, the Cas protein is part of a fusion protein (e.g., a fusion protein comprising (i) the Cas protein and (ii) a heterologous polypeptide).

In one aspect, the present invention provides a method for targeting a Cas protein to two or more target polynucleotides. The method comprises contacting the Cas protein with a set of guide RNA molecules described herein. In certain embodiments, the method results in formation of a guide RNA:Cas protein complex. In certain embodiments, the Cas protein is a wild type Cas9 protein. In certain embodiments, the Cas protein is a mutant or variant of a Cas9 protein. In certain embodiments, the Cas protein is a Cas protein having a single-strand nicking activity. In certain embodiments, the Cas protein is a Cas protein lacking nuclease activity (e.g., a nuclease-deficient mutant of Cas protein). In certain embodiments, the Cas protein is part of a fusion protein (e.g., a fusion protein comprising (i) the Cas protein or and (ii) a heterologous polypeptide).

In certain embodiments, the guide RNA is introduced into a cell by transfection. Techniques for RNA transfection are known in the art and include electroporation and lipofection. Effective techniques for RNA transfection depend mostly on cell type. See, e.g., Lujambio et al. (Spanish National Cancer Centre) *Cancer Res*. February 2007, which describes transfection of HTC-116 colon cancer cells and uses Oligofectamine (Invitrogen) for transfection of commercially obtained, modified miRNA or precursor miRNA. See also, Cho et al. (Seoul National Univ.) *Nat. Biotechnol*. March 2013, which describes transfection of K562 cells and uses 4D Nucleofection™ (Lonza) electroporation for transfection of transcribed sgRNAs (about 60 nts long). Techniques for transfection of RNA are also known in the art. For example, therapeutic RNA has been delivered in non-pathogenic *E. coli* coated with Invasin protein (to facilitate uptake into cells expressing β-1 integrin protein) and with the *E. coli* encoded to express lysteriolysin O pore-forming protein to permit the shRNA to pass from the *E. coli* into the cytoplasm. See also Cho et al. (Seoul National Univ.) *Nat. Biotechnol. March* 2013.

In certain embodiments, the guide RNA is introduced or delivered into cells. Technologies that can be used for delivery of guide RNA include those that utilize encapsulation by biodegradable polymers, liposomes, or nanoparticles. Such polymers, liposomes, and nanoparticles can be delivered intravenously. In certain embodiments, for in vivo delivery, guide RNA can be injected into a tissue site or administered systemically. In vivo delivery can also be effected by a beta-glucan delivery system, such as those described in U.S. Pat. Nos. 5,032,401 and 5,607,677, and U.S. Publication No. 2005/0281781, which are hereby incorporated by reference in their entirety. In certain embodiments, guide RNA or a delivery vehicle containing guide RNA is targeted to a particular tissue or body compartment. For example, in certain embodiments, to target exogenous RNA to other tissues, synthetic carriers are decorated with cell-specific ligands or aptamers for receptor uptake, e.g., RNA encased in cyclodextrin nanoparticles coated with PEG and functionalized with human transferrin protein for uptake via the transferrin receptor which is highly expressed in tumor cells. Further approaches are described herein below or known in the art.

The present invention has been tested in human cells as described in Hendel et al., *Nat. Biotechnol.* (2015) 33:9, 985-9 (which is incorporated in this application in its entirety). In the cited work, modified guide RNA was introduced into K562 cells, human primary T cells, and CD34+ hematopoietic stem and progenitor cells (HSPCs). The modified guide RNA significantly enhanced genome editing efficiencies in human cells, including human primary T cells and CD34+ HSPCs as compared to unmodified guide RNA.

FIGS. **11**A and **11**B illustrate experimental results showing that gene disruption in human cell lines can be achieved by high frequencies of indels or by cleavage-stimulated homologous recombination using synthesized and chemically modified sgRNAs disclosed herein. Gene disruption by mutagenic NHEJ was measured by deep sequencing of PCR amplicons (FIG. **12**A) or gene addition by HR at the three loci IL2RG, HBB and CCR5 in K562 cells induced by Cas9 in combination with synthetic sgRNAs (FIG. **12**B). The synthetic sgRNAs were delivered at 1 μg (light shade) or 20 μg (dark shade) per 1 million cells. Cas9 was expressed from a plasmid (2 μg) and for HR experiments 5 μg of GFP-encoding donor plasmid was included. As a positive control, 2 μg of sgRNA plasmid encoding both the sgRNA and the Cas9 protein was used (gray bars). Bars represent average values+s.e.m., n=3.

FIGS. **12**A, **12**B, **12**C and **12**D illustrate experimental results showing that chemically modified sgRNAs as described herein can be used to achieve high frequencies of gene disruption or targeted genome editing in stimulated primary human T cells and CD34+ hematopoietic stem and progenitor cells (HSPCs).

FIG. **12**A illustrates results from primary human T cells nucleofected with 10 μg of a synthetic CCR5 sgRNAs and either 15 μg Cas9 mRNA or 1 μg Cas9-encoding plasmid. 1 μg sgRNA plasmid encoding both the sgRNA and Cas9 protein was included for comparison. The bars represent average indel frequencies for three different donors+s.e.m., n=6, as measured by TIDE (tracking of indels by decomposition) analysis of PCR amplicons spanning the sgRNA target site, and using a mock-treated sample as control reference. Delivery of Cas9 mRNA with the unmodified or the M-modified sgRNA, and nucleofection of the plasmid encoding both the sgRNA and Cas9, did not give rise to allele modification frequencies above background. Co-transfection of the MSP-modified sgRNA with DNA expression plasmid for Cas9 generated 9.3% indel frequency. Cas9

mRNA with either the MS- or MSP-modified sgRNA generated 48.7% and 47.9% indel frequencies, respectively.

FIG. **12**B illustrates results from stimulated T cells. The cells were nucleofected as above, but with 15 μg Cas9 protein complexed with a 2.5 molar excess of the indicated synthetic CCR5 sgRNAs. Indel frequencies were measured by TIDE analysis. The bars represent average indel frequencies for three different donors+s.e.m., n=6. A 2.4-fold improvement in indel frequencies of the MS-modified sgRNA over the unmodified sgRNA (30.7% vs. 12.8%) was observed for chemically modified sgRNAs when delivered complexed with Cas9 protein. These results establish that chemically modified sgRNAs can be used for genome editing of stimulated T cells when delivered complexed with Cas9 protein.

FIG. **12**C illustrates results from human peripheral blood CD34+HSPCs. 500,000 mobilized cells were nucleofected with 10 μg of the indicated synthetic sgRNAs targeting IL2RG or HBB and either 15 μg Cas9 mRNA or 1 μg Cas9 plasmid. 1 μg of sgRNA plasmid encoding both the sgRNA and Cas9 protein was included for comparison. Bars represent average indel frequencies+s.e.m., n=3, as measured by T7 endonuclease cleavage assay. Indels were not detected at either locus using the unmodified or M-modified sgRNAs when co-transfected with Cas9 mRNA. However, the IL2RG MS- and MSP-modified sgRNAs showed 17.5% and 17.7% indel frequencies, respectively, and 23.4% and 22.0%, respectively, for the HBB MS- and MSP-modified sgRNAs.

FIG. **12**D illustrates results from stimulated T cells or mobilized human peripheral blood CD34+ HSPCs. One million cells were nucleofected with 15 μg Cas9 mRNA and 10 μg of the indicated synthetic CCR5 sgRNAs. A recent study showed that the simultaneous use of two sgRNAs could improve gene disruption in human primary T cells and in CD34+ HSPCs. See, e.g., Mandal et al. (2014) *Cell Stem Cell,* 15, 643-52. MS- and MSP-modified CCR5 sgRNAs were chemically synthesized with the sequences reported in Mandal study (termed 'D' and 'Q'), which cut 205 base pairs apart. When used in combination, the amount of each sgRNA was 5 μg. Indel frequencies for samples with single sgRNAs were measured by TIDE analysis as above and allele disruption frequencies for samples with two sgRNAs were measured by sequencing of cloned PCR products. The bars represent average indel frequencies+s.e.m., n=3. In T cells, the 'D' sgRNA alone gave rise to 56.0% and 56.3% indels for the MS- and MSP-modified sgRNA, respectively, and the 'Q' sgRNA gave rise to 62.6% and 69.6% indels, respectively. When used in combination, the frequencies of allele modification increased, as we observed 73.9% and 93.1% indels for the MS- and MSP-modified sgRNAs, respectively, of which the majority of the modification events were deletions between the two sgRNA target sites. In CD34+HSPCs, observations were similar though the overall frequencies were lower. For the 'D' sgRNA, allele modification frequencies of 9.8% and 11.2% were observed for the MS- and MSP-modified sgRNA, respectively, and 17.8% and 19.2% for the 'Q' sgRNA. When used in combination the frequencies increased to 37.8% and 43.0% for the MS- and MSP-modified sgRNAs, respectively. This shows that the use of two chemically modified sgRNAs is a highly effective way to facilitate gene disruption in primary human T cells and CD34+ HSPCs.

Examples of other uses include genomic editing and gene expression regulation as described below.

Genomic Editing

In one aspect, the present invention provides a method for genomic editing to modify a DNA sequence in vivo or in vitro ("in vitro" includes, without being limited to, a cell-free system, a cell lysate, an isolated component of a cell, and a cell outside of a living organism). The DNA sequence may comprise a chromosomal sequence, an episomal sequence, a plasmid, a mitochondrial DNA sequence, or a functional intergenic sequence, such as an enhancer sequence or a DNA sequence for a non-coding RNA. The method comprises contacting the DNA sequence with (i) a guide RNA or a set of guide RNA molecules described herein, and (ii) a Cas protein. In certain embodiments, the DNA sequence is contacted outside of a cell. In certain embodiments, the DNA sequence is located in the genome within a cell and is contacted in vitro or in vivo. In certain embodiments, the cell is within an organism or tissue. In certain embodiments, the cell is a human cell, a non-human mammalian cell, a stem cell, a non-mammalian vertebrate cell, an invertebrate cell, a plant cell, a single cell organism, or an embryo. In certain embodiments, the guide RNA aids in targeting the Cas protein to a targeted site in the DNA sequence. In certain embodiments, the Cas protein cleaves at least one strand of the DNA sequence at the targeted site. In certain embodiments, the Cas protein cleaves both strands of the DNA sequence at the targeted site.

In certain embodiments, the method further comprises introducing the Cas protein into a cell or another system. In certain embodiments, the Cas protein is introduced as a purified or non-purified protein. In certain embodiments, the Cas protein is introduced via an mRNA encoding the Cas protein. In certain embodiments, the Cas protein is introduced via a linear or circular DNA encoding the Cas protein. In certain embodiments, the cell or system comprises a Cas protein or a nucleic acid encoding a Cas protein.

In certain embodiments, a double-stranded break can be repaired via an error-prone, non-homologous end-joining ("NHEJ") repair process. In certain embodiments, a double-stranded break can be repaired by a homology-directed repair (HDR) process such that a donor sequence in a donor polynucleotide can be integrated into or exchanged with the targeted DNA sequence.

In certain embodiments, the method further comprises introducing at least one donor polynucleotide into the cell or system. In certain embodiments, the donor polynucleotide comprises at least one homologous sequence having substantial sequence identity with a sequence on either side of the targeted site in the DNA sequence. In certain embodiments, the donor polynucleotide comprises a donor sequence that can be integrated into or exchanged with the DNA sequence via homology-directed repair, such as homologous recombination.

In certain embodiments, the donor polynucleotide includes an upstream homologous sequence and a downstream homologous sequence, each of which have substantial sequence identity to sequences located upstream and downstream, respectively, of the targeted site in the DNA sequence. These sequence similarities permit, for example, homologous recombination between the donor polynucleotide and the targeted DNA sequence such that the donor sequence can be integrated into (or exchanged with) the DNA sequence targeted.

In certain embodiments, the target site(s) in the DNA sequence spans or is adjacent to a mutation, e.g., point mutation, a translocation or an inversion which may cause or be associated with a disorder. In certain embodiments, the method comprises correcting the mutation by introducing into the cell or system at least one donor polynucleotide

comprising (i) a wild type counterpart of the mutation and (ii) at least one homologous sequence having substantial sequence identity with a sequence on one side of the targeted site in the DNA sequence. In certain embodiments, the donor polynucleotide comprises a homologous sequence having substantial sequence identity with a sequence on both sides of the targeted site in the DNA sequence.

In certain embodiments, the donor polynucleotide comprises an exogenous sequence that can be integrated into or exchanged with the targeted DNA sequence via a homology-directed repair process, such as homologous recombination. In certain embodiments, the exogenous sequence comprises a protein coding gene, which, optionally, is operably linked to an exogenous promoter control sequence. Thus, in certain embodiments, upon integration of the exogenous sequence, a cell can express a protein encoded by the integrated gene. In certain embodiments, the exogenous sequence is integrated into the targeted DNA sequence such that its expression in the recipient cell or system is regulated by the exogenous promoter control sequence. Integration of an exogenous gene into the targeted DNA sequence is termed a "knock in." In other embodiments, the exogenous sequence can be a transcriptional control sequence, another expression control sequence, an RNA coding sequence, and the like.

In certain embodiments, the donor polynucleotide comprises a sequence that is essentially identical to a portion of the DNA sequence at or near the targeted site, but comprises at least one nucleotide change. For example, in certain embodiments, the donor sequence comprises a modified or mutated version of the DNA sequence at or near the targeted site such that, upon integration or exchange with the targeted site, the resulting sequence at the targeted site comprises at least one nucleotide change. In certain embodiments, the at least one nucleotide change is an insertion of one or more nucleotides, a deletion of one or more nucleotides, a substitution of one or more nucleotides, or combinations thereof. As a consequence of the integration of the modified sequence, the cell may produce a modified gene product from the targeted DNA sequence.

In certain embodiments, the methods are for multiplex applications. In certain embodiments, the methods comprise introducing a library of guide RNAs into the cell or system. In certain embodiments, the library comprises at least 100 unique guide sequences. In certain embodiments, the library comprises at least 1,000 unique guide sequences. In certain embodiments, the library comprises at least 10,000 unique guide sequences. In certain embodiments, the library comprises at least 100,000 unique guide sequences. In certain embodiments, the library comprises at least 1,000,000 unique guide sequences. In certain embodiments, the library targets at least 10 different polynucleotides or at least 10 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 100 different polynucleotides or at least 100 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 1,000 different polynucleotides or at least 1,000 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 10,000 different polynucleotides or at least 10,000 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 100,000 different polynucleotides or at least 100,000 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 1,000,000 different polynucleotides or at least 1,000,000 different sequences within one or more polynucleotides.

Genomic Editing in Human and Mammalian Cells

Embodiments of the present invention are useful in methods for genomic editing to modify a target polynucleotide, for example a DNA sequence, in a mammalian cell.

In certain embodiments, the DNA sequence is a chromosomal sequence. In certain embodiments, the DNA sequence is a protein-coding sequence. In certain embodiments, the DNA sequence is a functional intergenic sequence, such as an enhancer sequence or a non-coding sequence. In certain embodiments, the DNA is part of a human gene. In some such embodiments, the human gene is the clathrin light chain (CLTA1) gene, the human interleukin 2 receptor gamma (IL2RG) gene, the human cytotoxic T-lymphocyte-associated protein 4 (CLTA4) gene, the human protocadherin alpha 4 (PCDHA4) gene, the human engrailed homeobox 1 (EN1) gene), the human hemoglobin beta (HBB) gene, which can harbor mutations responsible for sickle cell anemia and thalassemias, or the human chemokine (C-C motif) receptor 5 (CCR5) gene which encodes a co-receptor of HIV.

In certain embodiments, the mammalian cell is a human cell. In some such embodiments, the human cell is a primary human cell. In further embodiments, the primary human cell is a human primary T cell. The human primary T cell may be stimulated or unstimulated. In certain embodiments, the human cell is a stem/progenitor cell, such as a CD34+ hematopoietic stem and progenitor cell (HSPC). In certain embodiments, the human cell is from a cultured cell line, for example such as can be obtained commercially. Exemplary cell lines include K562 cells, a human myelogenous leukemia line.

In certain embodiments, the cell is within a living organism. In certain other embodiments, the cell is outside of a living organism.

The method comprises contacting the DNA sequence with (i) a guide RNA or a set of guide RNA molecules described herein, and (ii) a Cas protein.

In certain embodiments, the method further comprises introducing or delivering the guide RNA into the cell. In some such embodiments, the guide RNA is introduced into a cell by transfection. Techniques for RNA transfection are known in the art and include electroporation and lipofection. In other embodiments, the guide RNA is introduced into a cell (and, more particularly, a cell nucleus) by nucleofection. Techniques for nucleofection are known in the art and may utilize nucleofection devices such as the Lonza Nucleofector 2b or the Lonza 4D-Nucleofector and associated reagents.

In certain embodiments, the method further comprises introducing or delivering the Cas protein into the cell. In some such embodiments, the Cas protein is introduced as a purified or non-purified protein. In other embodiments, the Cas protein is introduced via an mRNA encoding the Cas protein. In some such embodiments, the mRNA encoding the Cas protein is introduced into the cell by transfection. In other embodiments, the mRNA encoding the Cas protein is introduced into a cell (and, more particularly, a cell nucleus) by nucleofection.

In certain embodiments, the method employs ribonucleoprotein (RNP)-based delivery such that the Cas protein is introduced into the cell in a complex with the guide RNA. For example, a Cas9 protein may be complexed with a guide RNA in a Cas9:gRNA complex, which allows for co-delivery of the gRNA and Cas protein. For example, the Cas:gRNA complex may be nucleofected into cells.

In certain embodiments, the method employs an all-RNA delivery platform. For example, in some such embodiments, the guide RNA and the mRNA encoding the Cas protein are

introduced into the cell simultaneously or substantially simultaneously (e.g., by co-transfection or co-nucleofection). In certain embodiments, co-delivery of Cas mRNA and modified gRNA results in higher editing frequencies as compared to co-delivery of Cas mRNA and unmodified gRNA. In particular, gRNA having 2'-O-methyl-3'-phosphorothioate (MS), or 2'-O-methyl-3'-thioPACE (MSP) incorporated at three terminal nucleotides at both the 5' and 3' ends, provide higher editing frequencies as compared to unmodified gRNA.

In certain embodiments, the guide RNA and the mRNA encoding the Cas protein are introduced into the cell sequentially; that is, the guide RNA and the mRNA encoding the Cas protein are introduced into the cell at different times. The time period between the introduction of each agent may range from a few minutes (or less) to several hours or days. For example, in some such embodiments, gRNA is delivered first, followed by delivery of Cas mRNA 4, 8, 12 or 24 hours later. In other such embodiments, Cas mRNA is delivered first, followed by delivery of gRNA 4, 8, 12 or 24 hours later. In some particular embodiments, delivery of modified gRNA first, followed by delivery of Cas mRNA results in higher editing frequencies as compared to delivery of unmodified gRNA followed by delivery of Cas mRNA.

In certain embodiments, the gRNA is introduced into the cell together with a DNA plasmid encoding the Cas protein. In some such embodiments, the gRNA and the DNA plasmid encoding the Cas protein are introduced into the cell by nucleofection. In some particular embodiments, an RNP-based delivery platform or an all-RNA delivery platform provides lower cytotoxicity in primary cells than a DNA plasmid-based delivery system.

In certain embodiments, the method provides significantly enhanced genome editing efficiencies in human cells, including human primary T cells and CD34+HSPCs.

In certain embodiments, modified gRNA increases the frequency of insertions or deletions (indels), which may be indicative of mutagenic NHEJ and gene disruption, relative to unmodified gRNA. In particular, modified gRNA having 2'-O-methyl-3'-phosphorothioate (MS) or 2'-O-methyl-3'-thioPACE (MSP) incorporated at three terminal nucleotides at both the 5' and 3' ends, increases the frequency of indels relative to unmodified gRNA.

In certain embodiments, co-delivery of modified gRNA and Cas mRNA to human primary T cells increases the frequency of indels as compared to co-delivery of unmodified gRNA and Cas mRNA. In particular, modified gRNA having 2'-O-methyl-3'-phosphorothioate (MS) or 2'-O-methyl-3'-thioPACE (MSP) incorporated at three terminal nucleotides at both the 5' and 3' ends, increases the frequency of indels in human primary T cells relative to unmodified gRNA.

In certain embodiments, modified gRNA improves gRNA stability relative to unmodified gRNA. As one example, gRNA having 2'-O-methyl (M) incorporated at three terminal nucleotides at both the 5' and 3' ends, modestly improves stability against nucleases and also improves base pairing thermostability over unmodified gRNA. As another example, gRNA having 2'-O-methyl-3'-phosphorothioate (MS) or 2'-O-methyl-3'-thioPACE (MSP) incorporated at three terminal nucleotides at both the 5' and 3' ends, dramatically improves stability against nucleases relative to unmodified gRNA. It is contemplated that gRNA end modifications enhance intracellular stability against exonucleases, thus enabling increased efficacy of genome editing when Cas mRNA and gRNA are co-delivered or sequentially delivered into human cells.

In certain embodiments, modified gRNA stimulates gene targeting, which, in turn, allows for gene editing by, for example, homologous recombination or NHEJ. In particular, gRNA having 2'-O-methyl-3'-phosphorothioate (MS), or 2'-O-methyl-3'-thioPACE (MSP) incorporated at three terminal nucleotides at both the 5' and 3' ends, stimulates higher levels of homologous recombination than unmodified gRNA.

In certain embodiments, modified gRNA retains high specificity. In certain embodiments, the ratio of on-target to off-target indel frequencies is improved with modified gRNA as compared to unmodified gRNA. In certain embodiments, modified gRNA delivered in an RNP complex with a Cas protein provides significantly better on-target: off-target ratios compared to a DNA plasmid-based delivery system.

Gene Expression Regulation

In certain embodiments, the guide RNA described herein is used for regulating transcription or expression of a gene of interest. For example, in certain embodiments, a fusion protein comprising a Cas protein (e.g., a nuclease-deficient Cas9) and a transcription activator polypeptide is used to increase transcription of a gene. Similarly, in certain embodiments, a fusion protein comprising a Cas protein (e.g., a nuclease-deficient Cas9) and a repressor polypeptide is used to knock-down gene expression by interfering with transcription of the gene.

In at least one aspect, the present invention provides a method for regulating the expression of a gene of interest in vivo or in vitro. The method comprises introducing into a cell or another system (i) a synthetic guide RNA described herein, and (ii) a fusion protein. In certain embodiments, the fusion protein comprises a Cas protein and an effector domain, such as a transcriptional activation domain, a transcriptional repressor domain, or an epigenetic modification domain. In certain embodiments, the fusion protein comprises a mutated Cas protein, such as a Cas9 protein that is a null nuclease. In certain embodiments, the Cas protein contains one or more mutations, such as D10A, H840A and/or N863A.

In certain embodiments, the fusion protein is introduced into the cell or system as a purified or non-purified protein. In certain embodiments, the fusion protein is introduced into the cell or system via an mRNA encoding the fusion protein. In certain embodiments, the fusion protein is introduced into the cell or system via a linear or circular DNA encoding the fusion protein.

In certain embodiments, the guide RNA aids in directing the fusion protein to a specific target polynucleotide comprising a chromosomal sequence, an episomal sequence, a plasmid, a mitochondrial DNA sequence, or a functional intergenic sequence, such as an enhancer or the DNA sequence for a non-coding RNA. In certain embodiments, the effector domain regulates expression of a sequence in the target polynucleotide. A guide RNA for modulating gene expression can be designed to target any desired endogenous gene or sequence encoding a functional RNA. A genomic target sequence can be selected in proximity of the transcription start site of the endogenous gene, or alternatively, in proximity of the translation initiation site of the endogenous gene. In certain embodiments, the target sequence is in a region of the DNA that is traditionally termed the "promoter proximal" region of a gene. In certain embodiments, the target sequence lies in a region from about 1,000 base pairs upstream of the transcription start site to about 1,000 base pairs downstream of the transcription start site. In

certain embodiments, the target sequence is remote from the start site for transcription of the gene (e.g., on another chromosome).

In certain embodiments, the methods are for multiplex applications. In certain embodiments, the methods comprise introducing a library of guide RNAs into the cell or system. In certain embodiments, the library comprises at least 100, at least 1,000, at least 10,000, at least 100,000, or at least 1,000,000 unique guide sequences. In certain embodiments, the library targets at least 10 different polynucleotides or at least 10 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 100 different polynucleotides or at least 100 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 1,000 different polynucleotides or at least 1,000 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 10,000 different polynucleotides or at least 10,000 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 100,000 different polynucleotides or at least 100,000 different sequences within one or more polynucleotides. In certain embodiments, the library targets at least 1,000,000 different polynucleotides or at least 1,000,000 different sequences within one or more polynucleotides.

Kits

In one aspect, the present invention provides kits containing reagents for performing the above-described methods, including producing gRNA:Cas protein complex and/or supporting its activity for binding, nicking or cleaving target polynucleotide. In certain embodiments, one or more of the reaction components, e.g., one or more guide RNAs and Cas proteins, for the methods disclosed herein, can be supplied in the form of a kit for use. In certain embodiments, the kit comprises a Cas protein or a nucleic acid encoding the Cas protein, and one or more guide RNAs described herein or a set or library of guide RNAs. In certain embodiments, the kit includes one or more other reaction components. In certain embodiments, an appropriate amount of one or more reaction components is provided in one or more containers or held on a substrate.

Examples of additional components of the kits include, but are not limited to, one or more different polymerases, one or more host cells, one or more reagents for introducing foreign nucleic acid into host cells, one or more reagents (e.g., probes or PCR primers) for detecting expression of the guide RNA and/or the Cas mRNA or protein or for verifying the status of the target nucleic acid, and buffers, transfection reagents or culture media for the reactions (in 1× or more concentrated forms). In certain embodiments, the kit includes one or more of the following components: biochemical and physical supports; terminating, modifying and/or digesting reagents; osmolytes; and apparati for reaction, transfection and/or detection.

The reaction components used can be provided in a variety of forms. For example, the components (e.g., enzymes, RNAs, probes and/or primers) can be suspended in an aqueous solution or bound to a bead or as a freeze-dried or lyophilized powder or pellet. In the latter case, the components, when reconstituted, form a complete mixture of components for use in an assay. The kits of the invention can be provided at any suitable temperature. For example, for storage of kits containing protein components or complexes thereof in a liquid, it is preferred that they are provided and maintained below 0° C., preferably at about −20° C., possibly in a freeze-resistant solution containing glycerol or other suitable antifreeze.

A kit or system may contain, in an amount sufficient for at least one assay, any combination of the components described herein. In some applications, one or more reaction components may be provided in pre-measured single use amounts in individual, typically disposable, tubes or equivalent containers. With such an arrangement, a RNA-guided nuclease reaction can be performed by adding a target nucleic acid, or a sample or cell containing the target nucleic acid, to the individual tubes directly. The amount of a component supplied in the kit can be any appropriate amount and may depend on the market to which the product is directed. The container(s) in which the components are supplied can be any conventional container that is capable of holding the supplied form, for instance, microfuge tubes, microtiter plates, ampoules, bottles, or integral testing devices, such as fluidic devices, cartridges, lateral flow, or other similar devices.

The kits can also include packaging materials for holding the container or combination of containers. Typical packaging materials for such kits and systems include solid matrices (e.g., glass, plastic, paper, foil, micro-particles and the like) that hold the reaction components or detection probes in any of a variety of configurations (e.g., in a vial, microtiter plate well, microarray, and the like). The kits may further include instructions recorded in a tangible form for use of the components.

EXAMPLES

Example 1

To evaluate the ability of the chemically synthesized guide RNAs to target and cleave a DNA target sequence, an in vitro cleavage assay was developed. Briefly, as shown in FIG. **3**, ~4-kb PAM-addressable DNA targets were prepared by preparative PCR amplification of plasmid-borne human sequences (here, a sequence from the human clathrin light chain CLTA gene). In a 20-uL reaction volume, 50 fmoles of linearized DNA target in the presence of 50 nM sgRNA, 39 nM recombinant purified Cas9 protein (*S. pyogenes*; Agilent) and 10 mM $MgCl_2$ at pH 7.6 was incubated at 37° C. for 30 min. Upon completion, 0.5 uL of RNace It (Agilent) was added, and incubation was continued at 37° C. for 5 min and then at 70° C. for 15 min. Subsequently 0.5 μL of Proteinase K (Mol. Bio. grade, NEB) was added and incubated at 37° C. for 15 min. Aliquots were loaded into a DNA 7500 LabChip and were analyzed on a Bioanalyzer 2200. The workup steps served to release Cas9 from binding to target DNA, which were assayed for cleavage.

A series of guide RNAs as listed in FIG. **4** were chemically synthesized. Briefly, individual RNA strands were synthesized and HPLC purified. All oligonucleotides were quality control approved on the basis of chemical purity by HPLC analysis and full-length strand purity by mass spectrometry analysis. Each of these guide RNAs was designed to target the human CLTA gene.

The results are shown in FIG. **4**. As shown in the Table 1 of FIG. **4**, all but one of the chemically synthesized guide RNAs targeted and cleaved the CLTA-encoded DNA target sequence with significant cleavage rates. The one exception was "CLTA_37_Deoxy" guide RNA, which had a contiguous sequence of 37 deoxyribonucleotides at its 5' end.

As disclosed herein, a variety of chemical modifications were tested at specific positions in the sequence of a guide RNA. Surprisingly, the tested positions in the guide sequence of the guide RNA (a.k.a. the spacer sequence in the guide RNA) tolerated most of the modifications tested,

including combinations of multiple modifications within single nucleotides in the guide RNA, even when modifications were instantiated in the target-binding sequences.

The results revealed that guide RNAs containing modifications at specific positions were tolerated by active Cas protein and gRNA:Cas protein complexes, as the modifications did not prevent target-specific cleavage of the target polynucleotide. In all the guide RNA sequences listed in the Table 1 of FIG. **4**, the first 20 nucleotides at the 5' end are complementary to the target sequence in target DNA. The modifications that were tested and found to be tolerated at specific positions include 2'-O-methylribonucleotide (=2'OMe), 2'-deoxyribonucleotide, racemic phosphorothioate internucleotide linkage(s) (=P(S)), 3'-phosphonoacetate (=PACE), 3'-thiophosphonoacetates (=thioPACE), Z nucleotides, and combinations of these.

It is contemplated that the chemical modifications disclosed and tested herein, particularly at the tested positions (as listed in the Table 1 of FIG. **4**), will be tolerated at equivalent positions in a variety of guide RNAs. In certain embodiments, the chemical modifications disclosed and tested herein are tolerated in any position in a guide RNA.

As disclosed herein, chemically modified nucleotides were incorporated into guide RNAs in an effort to improve certain properties. Such properties include improved nuclease resistance of the guide RNA, reduced off-target effects of a gRNA:Cas protein complex (also known as improved specificity), improved efficacy of gRNA:Cas protein complex when cleaving, nicking or binding a target polynucleotide, improved transfection efficiency, and/or improved organelle localization such as nuclear localization.

While the use of modified RNA is known (e.g., to block nucleotlytic degradation in certain applications), it is widely known that one cannot simply incorporate modifications at any or all positions in an RNA sequence and expect it to function, particularly when the RNA sequence needs to complex with a protein or an enzyme to exert certain functions. Thus, it was not predictable whether these guide RNAs could tolerate chemical modifications at a variety of nucleotide positions while performing sufficient or improved function in a CRISPR-Cas system. In fact, it was unexpected that the guide RNA can tolerate specific modifications to the extent instantiated and tested, especially at several of the positions tested.

Example 2

To evaluate the ability of the chemically synthesized guide RNAs to target and cleave a DNA target sequence, an in vitro cleavage assay similar to that described in Example 1 was used. Target DNA constructs were for human DNA targets (sequences from the human clathrin light chain (CLTA1) gene, the human Interleukin 2 Receptor Gamma (IL2RG) gene, the human cytotoxic T-lymphocyte-associated protein 4 (CLTA4) gene, the human protocadherin alpha 4 (PCDHA4) gene, and the human engrailed homeobox 1 (EN1) gene), along with off-target DNA constructs differing from the target DNA by one or more nucleotides.

Table 3 sets forth the guide RNA constructs and their sequences, along with DNA constructs used for assessing the ability of those guide RNA constructs to target and cleave. In all the guide RNA sequences listed in the Table 3, the first 20 nucleotides at the 5' end are complementary to the target sequence in target DNA. ON target constructs comprise the 20 nt target sequence. OFF target constructs comprise most of the same 20 nucleotides as the target DNA, with 1, 2 or 3 nucleotide differences. Accordingly, the guide RNA is mostly, but not completely, complementary to the sequence of the OFF target constructs. The OFF target constructs are based on gene sequences known to occur in the human genome.

TABLE 3

2-piece dual-guide scaffold
Unmodified dual-guide RNA (dgRNA)

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
1	CLTA1 crRNA + tracrRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA	56 + 86
2	CLTA1 crRNA + tracrRNA	CLTA1 ON1-target	ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA	56 + 86
3	CLTA1 crRNA + tracrRNA	CLTA1 OFF1-target	ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA	56 + 86
4	CLTA1 crRNA + tracrRNA	CLTA1 OFF1-target	ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC + (SEQ ID NO: 25) GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA	56 + 86
5	CLTA1 crRNA + tracrRNA	CLTA1 OFF2-target	ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA	56 + 86
6	CLTA1 crRNA + tracrRNA	CLTA1 OFF2-target	ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA	56 + 86
7	CLTA1 crRNA + tracrRNA	CLTA1 OFF3-target	ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) +	−56 + 86
8	CLTA1 crRNA + tracrRNA	CLTA1 OFF3-target	GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) +	56 + 86
9	CLTA1 crRNA + tracrRNA	CLTA1 target	GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 25) +	56 + 86
10	IL2RG_crRNA + tracrRNA	IL2RGrrig ON-target	GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26) UGGUAAUGAUGGCUUCAACAGUUUUAGAGCUAUGCUGUUUUGAAUGGUCCCAAAAC (SEQ ID NO: 27) +	56 + 86
			GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 28)	

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
			Fluorophore-coupled dgRNA	
11	CLTA1 crRNA + tracrRNA_aminoallyl-U57 + Cy5	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGUCC CAAAAC (SEQ ID NO: 29) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUG(**aminoallylU + Cy5**)AAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 30)	56 + 86
			2'OMethyl-modified dgRNA	
12	IL2RG_crRNA_5', 3'-3x(2'OMe) + tracrRNA_5', 3'-3x(2'OMe)	IL2RGmg ON-target	**UGG**UAAUGAUGGCUUCAACAGUUUUAGAGCUAUGCUGUUUUGAAUGGUC CCA**AAA**C (SEQ ID NO: 31) + **GGA**ACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUU**UUU**U (SEQ ID NO: 32)	56 + 86
			2'OMethyl, 3'Phosphorothioate-modified dgRNA	
13	IL2RG_crRNA_5', 3'-3x(2'OMe, 3'P(S)) + tracrRNA_5', 3'-3x(2'OMe, 3'P(S))	IL2RGmg ON-target	**UsGsGs**UAAUGAUGGCUUCAACAGUUUUAGAGCUAUGCUGUUUUGAAUGG UCCCA**AsAsAs**C (SEQ ID NO: 33) + **GsGsAs**ACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAU CAACUUGUAAAAGUGGCACCGAGUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 34)	56 + 86
			2'OMethyl, 3'PhosphorothioPACE-modified dgRNA	
14	IL2RG_crRNA_5', 3'-3x(2'OMe, 3'thioPACE) + tracrRNA_5', 3'-3x(2'OMe, 3'thioPACE)	IL2RGmg ON-target	**U*sG*sG*s**UAAUGAUGGCUUCAACAGUUUUAGAGCUAUGCUGUUUUGAAU GGUCCCA**A*sA*sA*s**C (SEQ ID NO: 35) + **G*sG*sA*s**ACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGU UAUCAACUUGUAAAAGUGGCACCGAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 36)	56 + 86
15	IL2RG_crRNA_5', 3'-1x(2'OMe, 3'thioPACE) + tracrRNA_5', 3'-1x(2'OMe, 3'thioPACE)	IL2RGmg ON-target	**U*s**GGUAAUGAUGGCUUCAACAGUUUUAGAGCUAUGCUGUUUUGAAUGGU CCCAAA**A*s**C (SEQ ID NO: 37) + **G*s**GAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAU CAACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUU**U*s**U (SEQ ID NO: 38)	56 + 86
			2-thioU-modified dgRNA	
16	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 ON1-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
17	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 ON1-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
18	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 OFF1-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
19	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 OFF1-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
20	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 OFF2-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
21	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 OFF2-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
22	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 OFF3-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
23	CLTA1_2thioU + 3 crRNA + tracrRNA	CLTA1 OFF3-target	AG(**2sU**)CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 39) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
24	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 ON1-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
25	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 ON1-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
26	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 OFF1-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
27	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 OFF1-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
28	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 OFF2-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
29	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 OFF2-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
30	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 OFF3-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
31	CLTA1_2thioU + 9 crRNA + tracrRNA	CLTA1 OFF3-target	AGUCCUCA(**2sU**)CUCCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 40) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
32	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 ON1-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
33	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 ON1-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGU UUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
34	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 OFF1-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
35	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 OFF1-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGU UUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
36	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 OFF2-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
37	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 OFF2-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
38	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 OFF3-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
39	CLTA1_2thioU + 11 crRNA + tracrRNA	CLTA1 OFF3-target	AGUCCUCAUC(**2sU**)CCCUCAAGCGUUUAAGAGCUAUGCUGUUUUGAAUGGU CCCAAAAC (SEQ ID NO: 41) + GGAACCAUUCAAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCA ACUUGUAAAAGUGGCACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 26)	56 + 86
			Single-guide scaffold	
			Unmodified single-guide RNA (sgRNA)	
40	CLTA1 sgRNA (Batch #1)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
41	CLTA1 sgRNA (Batch #1)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
42	CLTA1 sgRNA (Batch #2)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
43	CLTA1 sgRNA (Batch #2)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
44	CLTA1 sgRNA (Batch #3)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
45	CLTA1 sgRNA (Batch #3)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
46	CLTA1 sgRNA (Batch #3)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
47	CLTA1 sgRNA (Batch #3)	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
48	CLTA1 sgRNA (Batch #3)	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
49	CLTA1 sgRNA (Batch #3)	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
50	CLTA1 sgRNA (Batch #3)	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
51	CLTA1 sgRNA (Batch #3)	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
52	CLTA1 sgRNA (crude)	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 42)	113
53	CLTA1_Bos sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 43)	100
54	CLTA1_Bos sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 43)	100
55	CLTA1_Bos sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 43)	100
56	CLTA1_Bos sgRNA	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 43)	100
57	CLTA1_Bos sgRNA	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 43)	100

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
58	CLTA4 sgRNA	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 44)	113
59	CLTA4 sgRNA	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 44)	113
60	CLTA4 sgRNA	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 44)	113
61	CLTA4 sgRNA	CLTA4mg ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 44)	113
62	CLTA4 sgRNA	CLTA4mg ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 44)	113
63	CLTA4 sgRNA	CLTA4mg OFF5-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 44)	113
64	CLTA1_Truncated_18 mer	CLTA1mg ON1-target	UCCUCAUCCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAG UUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUUUUUUU (SEQ ID NO: 45)	111
65	CLTA1_Truncated_18 mer	CLTA1mg ON1-target	UCCUCAUCCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAG UUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUUUUUUU (SEQ ID NO: 45)	111
66	CLTA1_Truncated_18 mer	CLTA1mg OFF1-target	UCCUCAUCCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAG UUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUUUUUUU (SEQ ID NO: 45)	111
67	CLTA1_Truncated_18 mer	CLTA1mg OFF3-target	UCCUCAUCCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAG UUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUUUUUUU (SEQ ID NO: 45)	111
68	CLTA1_Truncated_17 mer	CLTA1mg ON1-target	CCUCAUCCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAGU UUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGU GCUUUUUUU (SEQ ID NO: 46)	110
69	CLTA1_Truncated_17 mer	CLTA1mg ON1-target	CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAGU UUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGU GCUUUUUUU (SEQ ID NO: 46)	110
70	CLTA1_Truncated_17 mer	CLTA1mg OFF1-target	CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAGU UUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGU GCUUUUUUU (SEQ ID NO: 46)	110
71	CLTA1_Truncated_17 mer	CLTA1mg OFF3-target	CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCAAGU UUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGU GCUUUUUUU (SEQ ID NO: 46)	110
72	CLTA1_1xExtraG	CLTA1mg ON1-target	GAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 47)	114
73	CLTA1_1xExtraG	CLTA1mg ON1-target	GAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 47)	114

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
74	CLTA1_1xExtraG	CLTA1mg OFF1-target	GAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 47)	114
75	CLTA1_1xExtraG	CLTA1mg OFF3-target	GAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 47)	114
76	CLTA1_2xExtraG	CLTA1mg ON1-target	GGAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 48)	115
77	CLTA1_2xExtraG	CLTA1mg ON1-target	GGAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 48)	115
78	CLTA1_2xExtraG	CLTA1mg OFF1-target	GGAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 48)	115
79	CLTA1_2xExtraG	CLTA1mg OFF3-target	GGAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 48)	115
80	CLTA1_63U,64U	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAUUCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 49)	113
81	CLTA163A,64A	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAACUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 50)	113
82	CLTA1_63A,64A,70U,71U	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAACUAGUUUGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 51)	113
83	CLTA1_cis-block(1-5)_polyU_sgRNA	CLTA1mg ON1-target	GGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 52)	111
84	CLTA1_cis-block(1-5)_polyU_sgRNA	CLTA1mg ON1-target	GGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 52)	111
85	CLTA1_cis-block(1-5)_polyU_sgRNA	CLTA1mg OFF1-target	GGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 52)	111
86	CLTA1_cis-block(1-5)_polyU_sgRNA	CLTA1mg OFF3-target	GGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 52)	111
87	CLTA1_cis-block(1-10)_polyU_sgRNA	CLTA1mg ON1-target	GAUGAGGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGA AAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUUU (SEQ ID NO: 53)	116
88	CLTA1_cis-block(1-10)_polyU_sgRNA	CLTA1mg ON1-target	GAUGAGGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGA AAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUUU (SEQ ID NO: 53)	116
89	CLTA1_cis-block(1-10)_polyU_sgRNA	CLTA1mg OFF1-target	GAUGAGGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGA AAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUUU (SEQ ID NO: 53)	116

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
90	CLTA1_cis-block(1-10)_ polyU_sgRNA	CLTA1mg OFF3-target	GAUGAGGACUUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGA AAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUUU (SEQ ID NO: 53)	116
91	CLTA1_cis-block(16-20)_ polyU_sgRNA	CLTA1mg ON1-target	GCUUGUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 54)	111
92	CLTA1_cis-block(16-20)_ polyU_sgRNA	CLTA1mg ON1-target	GCUUGUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 54)	111
93	CLTA1_cis-block(16-20)_ polyU_sgRNA	CLTA1mg OFF1-target	GCUUGUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 54)	111
94	CLTA1_cis-block(16-20)_ polyU_sgRNA	CLTA1mg OFF3-target	GCUUGUUUUUUAGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGAAAUAG CAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUU (SEQ ID NO: 54)	111
			DMT-modified sgRNA	
95	CLTA1_DMT-ON sgRNA	CLTA1 ON1-target	(**dmt**)AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 55)	113
96	CLTA1_DMT-ON/OFF sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 56)	113
			Fluorophore-modified sgRNA	
97	CLTA1_IntFl_sgLoop	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 57)	113
98	CLTA1_IntFl_sgLoop	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 57)	113
99	CLTA1_IntFl_sgLoop	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 57)	113
100	CLTA1_IntFl_sgLoop	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 57)	113
101	CLTA1_IntFl_sgLoop	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 57)	113
102	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe)	CLTA1mg ON1-target	**AGU**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUU**UUU**U (SEQ ID NO: 58)	113
103	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe)	CLTA1mg ON1-target	**AGU**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUU**UUU**U (SEQ ID NO: 58)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
104	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe)	CLTA1mg OFF1-target	**AGU**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUU**UUU**U (SEQ ID NO: 58)	113
105	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe)	CLTA1mg OFF3-target	**AGU**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUU**UUU**U (SEQ ID NO: 58)	113
106	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg ON1-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 59)	113
107	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg ON1-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 59)	113
108	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg OFF1-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 59)	113
109	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg OFF3-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 59)	113
110	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg ON1-target	**A*sG*sU*s**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGC AUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCAC CGAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 60)	113
111	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg ON1-target	**A*sG*sU*s**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGC AUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCAC CGAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 60)	113
112	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg OFF1-target	**A*sG*sU*s**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGC AUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCAC CGAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 60)	113
113	CLTA1_IntFl_sgLoop_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg OFF3-target	**A*sG*sU*s**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGG(**Fl**)AACAGC AUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCAC CGAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 60)	113
114	CLTA4_3xFl-Int_3x(2'OMe, 3'thioPACE)	CLTA4mg ON-target	**Uo*s**(**Flo**)GCAGAUGUAGUGUUUCCACAGUUUaAGAGCUAGUAAUAGCAAGU UuAAAUAAGGCUAGUCCGUUA(Fl)CAACUUGAAAAAGUGGCACCGAGUCGG UGCU(**Fl**)**U*s**U (SEQ ID NO: 61)	102
115	CLTA4_3xFl-Int_3x(2'OMe, 3'thioPACE)	CLTA4mg OFF5-target	**Uo*s**(**Flo**)GCAGAUGUAGUGUUUCCACAGUUUaAGAGCUAGUAAUAGCAAGU UuAAAUAAGGCUAGUCCGUUA(Fl)CAACUUGAAAAAGUGGCACCGAGUCGG UGCU(**Fl**)**U*s**U (SEQ ID NO: 61)	102
116	CLTA4_3xFl-Loops_3x(2'OMe, 3'thioPACE)	CLTA4mg ON-target	**G*s**CAGAUGUAGUGUUUCCACAGUUUaAGAGCUAG(**Fl**)AAUAGCAAGUUuAA AUAAGGCUAGUCCGUUAUCAACUUG(**Fl**)AAAAGUGGCACCGAG(**Fl**)CGGUGC UU**U*s**U (SEQ ID NO: 62)	100
117	CLTA4_3xFl-Loops_3x(2'OMe, 3'thioPACE)	CLTA4mg OFF5-target	**G*s**CAGAUGUAGUGUUUCCACAGUUUaAGAGCUAG(**Fl**)AAUAGCAAGUUuAA AUAAGGCUAGUCCGUUAUCAACUUG(**Fl**)AAAAGUGGCACCGAG(**Fl**)CGGUGC UU**U*s**U (SEQ ID NO: 62)	100
		3'Phosphorothioate-modified sgRNA		
118	CLTA1_5'-2xP(S) sgRNA	CLTA1 ON1-target	AsGsUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 63)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
119	CLTA1_5'-3xP(S) sgRNA	CLTA1 ON1-target	AsGsUsCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 64)	113
120	CLTA1_5'-4xP(S) sgRNA	CLTA1 ON1-target	AsGsUsCsCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUUUUUU (SEQ ID NO: 65)	113
121	CLTA1_3'-4xP(S) sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGAAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUsUsUsUsU (SEQ ID NO: 66)	113
			2'OMethyl-modified sgRNA	
122	CLTA1_2'OMe + 20 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 67)	113
123	CLTA1_2'OMe + 19 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 68)	113
124	CLTA1_2'OMe + 19 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 68)	113
125	CLTA1_2'OMe + 19 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 68)	113
126	CLTA1_2'OMe + 19 sgRNA	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 68)	113
127	CLTA1_2'OMe + 19 sgRNA	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 68)	113
128	CLTA1_2'OMe + 18 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 69)	113
129	CLTA1_2'OMe + 18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 69)	113
130	CLTA1_2'OMe + 18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 69)	113
131	CLTA1_2'OMe + 18 sgRNA	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 69)	113
132	CLTA1_2'OMe + 18 sgRNA	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 69)	113
133	CLTA1_2'OMe + 17 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 70)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
134	CLTA1_2'OMe + 17 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 70)	113
135	CLTA1_2'OMe + 17 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 70)	113
136	CLTA1_2'OMe + 17 sgRNA	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 70)	113
137	CLTA1_2'OMe + 17 sgRNA	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 70)	113
138	CLTA1_2'OMe + 17,18 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 71)	113
139	CLTA1_2'OMe + 17,18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 71)	113
140	CLTA1_2'OMe + 17,18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 71)	113
141	CLTA1_2'OMe + 17,18 sgRNA	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 71)	113
142	CLTA1_2'OMe + 17,18 sgRNA	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 71)	113
143	CLTA1_5', 3'-3x(2'OMe) sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 72)	113
144	CLTA4_5', 3'-3x(2'OMe) sgRNA	CLTA4mg ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 73)	113
145	CLTA4_5', 3'-3x(2'OMe) sgRNA	CLTA4mg OFF5-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 73)	113
146	CLTA1_5'-2Ox(2'OMe) sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 74)	113
147	CLTA1_5'-2Ox(2'OMe) sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 74)	113
148	CLTA1_5'-2Ox(2'OMe) sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 74)	113
149	CLTA1_5'-2Ox(2'OMe) sgRNA	CLTA1mg OFF1 target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 74)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
150	CLTA1_5'-20x(2'OMe) sgRNA	CLTA1mg OFF3-target	**AGUCCUCAUCUCCCUCAAGC**GUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 74)	113
151	CLTA1_5'-26x(2'OMe) sgRNA	CLTA1 ON1-target	**AGUCCUCAUCUCCCUCAAGCGUUUAA**GAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 75)	113
152	CLTA1_5'-37x(2'OMe) sgRNA	CLTA1 ON1-target	**AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUG**GUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 76)	113
153	CLTA1_41x(2'OMeC/U)_ QB3	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 77)	113
154	CLTA1_47x(2'OMeC/U)_ QB3	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 78)	113
155	CLTA1_47x(2'OMeC/U)_ QB3	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 79)	113
156	CLTA1_47x(2'OMeC/U)_ QB3	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 79)	113
157	CLTA1_47x(2'OMeC/U)_ QB3	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 79)	113
158	CLTA1_47x(2'OMeC/U)_ QB3	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 79)	113
159	CLTA1_47x(2'OMeG/A)_ QB3	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 80)	113
160	CLTA1_47x(2'OMeG/A)_ QB3	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGA)AAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 80)	113
161	CLTA1_47x(2'OMeG/A)_ QB3	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 80)	113
162	CLTA1_47x(2'OMeG/A)_ QB3	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 80)	113
163	CLTA1_47x(2'OMeG/A)_ QB3	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 80)	113
164	CLTA1_43x(2'OMeG/A)_ Bos	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 81)	100
165	CLTA1_43x(2'OMeG/A)_ Bos	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 81)	100

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
166	CLTA1_43x(2'OMeG/A)_Bos	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 81)	100
167	CLTA1_43x(2'OMeG/A)_Bos	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 81)	100
168	CLTA1_43x(2'OMeG/A)_Bos	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAGCGUUUUAGAGCUAGUAAUAGCAAGUUAAAAUA AGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 81)	100
169	CLTA4 sgRNA_5', 3'-3x(2'OMe)	CLTA4 ON-target	**GCA**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUU**UUU**U (SEQ ID NO: 82)	113
170	CLTA4 sgRNA_5', 3'-3x(2'OMe)	CLTA4 ON-target	**GCA**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUU**UUU**U (SEQ ID NO: 82)	113
171	CLTA4_47x(2'OMeC/U)_QB3	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 83)	113
172	CLTA4_47x(2'OMeC/U)_QB3	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 83)	113
173	CLTA4_47x(2'OMeC/U)_QB3	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 83)	113
174	CLTA4_49x(2'OMeG/A)_Bos	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUUAGAGCUAGUAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 84)	100
175	CLTA4_49x(2'OMeG/A)_Bos	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUUAGAGCUAGUAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 84)	100
176	CLTA4_49x(2'OMeG/A)_Bos	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUUAGAGCUAGUAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 84)	100
177	CLTA4_39x(2'OMeC/U)_Bos	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUUAGAGCUAGUAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 85)	100
178	CLTA4_39x(2'OMeC/U)_Bos	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUUAGAGCUAGUAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 85)	100
179	CLTA4_39x(2'OMeC/U)_Bos	CLTA4 ON-target	GCAGAUGUAGUGUUUCCACAGUUUUAGAGCUAGUAAUAGCAAGUUAAAAU AAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU (SEQ ID NO: 85)	100
		2'Deoxy-modified sgRNA		
180	CLTA1_5'-20x(21deoxy)	CLTA1 ON1-target	**AGTCCTCATCTCCCTCAAGC**GUUUAAGAGCUAUGCUGGUAACAGCAUAGCAA GUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCG GUGCUUUUUUU (SEQ ID NO: 86)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
181	CLTA1_5'-26x(2'deoxy)	CLTA1 ON1-target	**AGTCCTCATCTCCCTCAAGCGTTTAA**GAGCUAUGCUGGUAACAGCAUAGCAAG UUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUUUUUUU (SEQ ID NO: 87)	113
182	CLTA1_5'-37x(2'deoxy)	CLTA1 ON1-target	**AGTCCTCATCTCCCTCAAGCGTTTAAGAGCTATGCTG**UAACAGCAUAGCAAG UUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGG UGCUUUUUUU (SEQ ID NO: 88)	113
			2'Deoxy, 3'PACE-modified sgRNA	
183	CLTA4_2'deoxy3'PACE + 15	CLTA4mg ON-target	GCAGAUGUAGUGUU**U***CCACAGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 89)	113
184	CLTA4_2'deoxy3'PACE + 15	CLTA4mg OFF5-target	GCAGAUGUAGUGUU**U***CCACAGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 89)	113
			2'OMethyl, 3'PACE-modified sgRNA	
185	5'-1x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	A*GUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 90)	113
186	5'-1x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	A*GUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 90)	113
187	5'-2x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1 ON1-target	A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 91)	113
188-	5'-2x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1 ON1-target	A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 91)	113
189	5'-2x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 91)	113
190	5'-2x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 91)	113
191	5'-3x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	G*G*A*GUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUUUUU (SEQ ID NO: 92)	115
192	5'-3x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	G*G*A*GUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUUUUU (SEQ ID NO: 92)	115
193	5'-4x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1 ON1-target	A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 93)	113
194	5'-4x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 93)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
195	5'-4x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 93)	113
196	5'-5x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	G*G*A*G*U*CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAG CAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUUUUUU (SEQ ID NO: 94)	115
197	5'-5x(2'OMe, 3'PACE)_CLTA1 sgRNA	CLTA1mg ON1-target	G*G*A*G*U*CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAG CAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA CCGAGUCGGUGCUUUUUUU (SEQ ID NO: 94)	115
198	CLTA1_3'-4x(2'OMe, 3'PACE) sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUU*U*U*U*U (SEQ ID NO: 95)	113
199	C LTA 1_3'-4x(2'OMe, 3'PACE) sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUU*U*U*U*U (SEQ ID NO: 95)	113
200	CLTA1_3'-4x(2'OMe, 3'PACE) sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUU*U*U*U*U (SEQ ID NO: 95)	113
201	CLTA1_3'-4x(2'OMe, 3'PACE) sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUU*U*U*U*U (SEQ ID NO: 95)	113
202	CLTA1 3'-5x(2'OMe, 3'PACE) sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUU*U*U*U*U*U (SEQ ID NO: 96)	113
203	CLTA1 3'-5x(2'OMe, 3'PACE) sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUU*U*U*U*U*U (SEQ ID NO: 96)	113
204	CLTA1_3'-5x(2'OMe, 3'PACE) sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUU*U*U*U*U*U (SEQ ID NO: 96)	113
205	CLTA1_3'-5x(2'OMe, 3'PACE) sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUU*U*U*U*U*U (SEQ ID NO: 96)	113
206	5'-3x(2'OMe, 3'PACE)_plus1 overhg_CLTA1	CLTA1 ON1-target	C$_o$*A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 97)	114
207	5'-3x(2'OMe, 3'PACE)_plus1 overhg_CLTA1	CLTA1mg ON1-target	C$_o$*A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 97)	114
208	5'-3x(2'OMe, 3'PACE)_plus1 overhg_CLTA1	CLTA1mg ON1-target	C$_o$*A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 97)	114
209	5'-3x(2'OMe, 3'PACE)_plus1 NC_overhg_CLTA1	CLTA1 ON1-target	G$_o$*A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 98	114
210	5'-3x(2'OMe, 3'PACE)_plus1 NC_overhg_CLTA1	CLTA1mg ON1-target	G$_o$*A*G*UCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: (SEQ ID NO: 98)	114

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
211	5'-3x(2'OMe, 3'PACE)_plus1 NC_overhg_CLTA1	CLTA1mg ON1-target	G$_o$*A*G*UCCUCAUCUCCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 98)	114
212	5'-5x(2'OMe, 3'PACE)_plus2 overhg_CLTA1	CLTA1 ON1-target	U$_o$*C$_o$*A*G*U*CCUCAUCUCCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACA GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGC ACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 99)	115
213	5'-5x(2'OMe, 3'PACE)_plus2 overhg_CLTA1	CLTA1mg ON1-target	U$_o$*C$_o$*A*G*U*CCUCAUCUCCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACA GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGC ACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 99)	115
214	5'-5x(2'OMe, 3'PACE)_plus2 overhg_CLTA1	CLTA1mg ON1-target	U$_o$*C$_o$*A*G*U*CCUCAUCUCCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACA GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGC ACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 99)	115
215	5'-5x(2'OMe, 3'PACE)_plus2 NC_overhg_CLTA1	CLTA1 ON1-target	A$_o$*G$_o$*A*G*U*CCUCAUCUCCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACA GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGC ACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 100)	115
216	5'-5x(2'OMe, 3'PACE)_plus2 NC_overhg_CLTA1	CLTA1mg ON1-target	A$_o$*G$_o$*A*G*U*CCUCAUCUCCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACA GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGC ACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 100)	115
217	5'-5x(2'OMe, 3'PACE)_plus2 NC_overhg_CLTA1	CLTA1mg ON1-target	A$_o$*G$_o$*A*G*U*CCUCAUCUCCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACA GCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGC ACCGAGUCGGUGCUUUUUUU (SEQ ID NO: 100)	115
218	5'-7x(2'OMe, 3'PACE)_plus3 overhg_CLTA1_3'-4x(2'OMe, 3'PACE)	CLTA1 ON1-target	C$_o$*U$_o$*C$_o$*A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUA ACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGU GGCACCGAGUCGGUGCUUU*U*U*U*U (SEQ ID NO: 101)	116
219	5'-7x(2'OMe, 3'PACE)_plus3 overhg_CLTA1_3'-4x(2'OMe, 3'PACE)	CLTA1mg ON1-target	C$_o$*U$_o$*C$_o$*A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUA ACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGU GGCACCGAGUCGGUGCUUU*U*U*U*U (SEQ ID NO: 101)	116
220	5'-7x(2'OMe, 3'PACE)_plus3 overhg_CLTA1_3'-4x(2'OMe, 3'PACE)	CLTA1mg ON1-target	C$_o$*U$_o$*C$_o$*A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUA ACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGU GGCACCGAGUCGGUGCUUU*U*U*U*U (SEQ ID NO: 101)	116
221	5'-7x(2'OMe, 3'PACE)_plus3 NC_overhg_CLTA1_3'-4x(2'OMe, 3'PACE)	CLTA1 ON1-target	G$_o$*A$_o$*G$_o$*A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUA ACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGU GGCACCGAGUCGGUGCUUU*U*U*U*U (SEQ ID NO: 101)	116
222	5'-7x(2'OMe, 3'PACE)_plus3 NC_overhg_CLTA1_3'-4x(2'OMe, 3'PACE)	CLTA1mg ON1-target	G$_o$*A$_o$*G$_o$*A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUA ACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGU GGCACCGAGUCGGUGCUUU*U*U*U*U (SEQ ID NO: 101)	116
223	5'-7x(2'OMe, 3'PACE)_plus3 NC_overhg_CLTA1_3'-4x(2'OMe, 3'PACE)	CLTA1mg ON1-target -	G$_o$*A$_o$*G$_o$*A*G*U*C*CUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUA ACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGU GGCACCGAGUCGGUGCUUU*U*U*U*U (SEQ ID NO: 101)	116
224	CLTA1_2'OMe, 3'PACE + 20 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGC*GUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 102	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
225	CLTA1_2'OMe, 3'PACE + 20 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGC*GUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 102)	113
226	CLTA1_2'OMe, 3'PACE + 20 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAGC*GUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 102)	113
227	CLTA1_2'OMePACE + 19 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAG*CGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 103)	113
228	CLTA1_2'OMePACE + 19 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAG*CGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 103)	113
229	CLTA1_2'OMePACE + 19 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAAG*CGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 103)	113
230	CLTA1_2'OMePACE + 19 sgRNA	CLTA1mg OFF1-target	AGUCCUCAUCUCCCUCAAG*CGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 103)	113
231	CLTA1_2'OMePACE + 19 sgRNA	CLTA1mg OFF3-target	AGUCCUCAUCUCCCUCAAG*CGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 103)	113
232	CLTA1_2'OMePACE + 18 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAA*GCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 104)	113
233	CLTA1_2'OMePACE + 18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAA*GCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 104)	113
234	CLTA1_2'OMePACE + 18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCAA*GCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 104)	113
235	CLTA1_2'OMePACE + 17 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCA*AGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 105)	113
236	CLTA1_2'OMePACE + 17 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCA*AGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 105)	113
237	CLTA1_2'OMePACE + 17 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCA*AGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 105)	113
238	CLTA1_2'OMePACE + 17,18 sgRNA	CLTA1 ON1-target	AGUCCUCAUCUCCCUCA*A*GCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 106)	113
239	CLTA1_2'OMePACE + 17,18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCA*A*GCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 106)	113
240	CLTA1_2'OMePACE + 17,18 sgRNA	CLTA1mg ON1-target	AGUCCUCAUCUCCCUCA*A*GCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUUUU (SEQ ID NO: 106)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
			2'OMethyl, 3'Phosphorothioate-modified sgRNA	
241	CLTA1_5', 3'-3x(2'OMe, 3'P(S))	CLTA1 ON1-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
242	CLTA1_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg ON1-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
243	CLTA1_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg ON1-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
244	CLTA1_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg OFF1-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
245	CLTA1_5', 3'-3x(2'OMe, 3'P(S))	CLTA1mg OFF3-target	**AsGsUs**CCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
246	CLTA4_5', 3'-3x(2'OMe, 3'P(S))	CLTA4 target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
247	CLTA4_5', 3'-3x(2'OMe, 3'P(S))	CLTA4 target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
248	CLTA4_5', 3'-3x(2'OMe, 3'P(S))	CLTA4mg ON-target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
249	CLTA4_5', 3'-3x(2'OMe, 3'P(S))	CLTA4mg ON-target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
250	CLTA4_5', 3'-3x(2'OMe, 3'P(S))	CLTA4mg ON-target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
251	CLTA4_5', 3'-3x(2'OMe, 3'P(S))	CLTA4mg OFF5-target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCUUU**UsUsUs**U (SEQ ID NO: 107)	113
252	CLTA4_5'-3x(2'OMe, 3'P(S)), 3'-5x(2'OMe, 3'P(S))	CLTA4mg ON-target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCU**UsUsUsUsUs**U (SEQ ID NO: 108)	113
253	CLTA4_5'-3x(2'OMe, 3'P(S)), 3'-5x(2'OMe, 3'P(S))	CLTA4mg ON-target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCU**UsUsUsUsUs**U (SEQ ID NO: 108)	113
254	CLTA4_5'-3x(2'OMe, 3'P(S)), 3'-5x(2'OMe, 3'P(S))	CLTA4mg ON-target	**GsCsAs**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGA GUCGGUGCU**UsUsUsUsUs**U (SEQ ID NO: 108)	113
255	CLTA4_5', 3'-5x(2'OMe, 3'P(S))	CLTA4mg ON-target	**GsCsAsGsAs**UGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCU**UsUsUsUsUs**U (SEQ ID NO: 109)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
256	CLTA4_5', 3'-5x(2'OMe, 3'P(S))	CLTA4mg ON-target	GsCsAsGsAsUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUsUsUsUsUsUsU (SEQ ID NO: 109)	113
257	CLTA4_5', 3'-5x(2'OMe, 3'P(S))	CLTA4mg OFF5-target	GsCsAsGsAsUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUsUsUsUsUsUsU (SEQ ID NO: 109)	113
		2'OMethyl, 3'PhosphorothioPACE-modified sgRNA		
258	CLTA1_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1 ON1-target	A*sG*sU*sCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUU*sU*sU*sU (SEQ ID NO: 110)	113
259	CLTA1_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg ON1-target	A*sG*sU*sCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUU*sU*sU*sU (SEQ ID NO: 110)	113
260	CLTA1_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg ON1-target	A*sG*sU*sCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUU*sU*sU*sU (SEQ ID NO: 110)	113
261	CLTA1_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg OFF1-target	A*sG*sU*sCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUU*sU*sU*sU (SEQ ID NO: 110)	113
262	CLTA1_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA1mg OFF3-target	A*sG*sU*sCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUU*sU*sU*sU (SEQ ID NO: 110)	113
263	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA1mg ON1-target	A*sGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU*sU (SEQ ID NO: 111)	113
264	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA1mg ON1-target	A*sGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU*sU (SEQ ID NO: 111)	113
265	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA1mg OFF1-target	A*sGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU*sU (SEQ ID NO: 111)	113
266	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA1mg OFF3-target	A*sGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU*sU (SEQ ID NO: 111)	113
267	CLTA1_5', 3'-3x(2'OMe, 3'thioPACE) _75 mer	CLTA1 ON1-target	A*sG*sU*sCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCG*sU*sU*sU (SEQ ID NO: 112)	75
268	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE) _74 mer	CLTA1mg ON1-target	A*sGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGU*sU (SEQ ID NO: 112)	74
269	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE) _75 mer	CLTA1mg ON1-target	A*sGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGU*sA (SEQ ID NO: 112)	75
270	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE) _77 mer	CLTA1mg ON1-target	A*sGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUA*sC (SEQ ID NO: 113)	77
271	CLTA1_5', 3'-1x(2'OMe, 3'thioPACE) _77 mer + G	CLTA1mg ON1-target	G*sAGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUA GCAAGUUUAAAUAAGGCUAGUCCGUUA*sC (SEQ ID NO: 114)	78
272	CLTA4_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA4 ON-target	G*sC*sA*sGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUUU*sU*sU*sU (SEQ ID NO: 115)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
273	CLTA4_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA4 ON-target	**G*sC*sA*s**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 115)	113
274	CLTA4_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA4 ON-target	**G*sC*sA*s**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 115)	113
275	CLTA4_5', 3'-3x(2'OMe, 3'thioPACE)	CLTA4mg OFF5-target	**G*sC*sA*s**GAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCA UAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACC GAGUCGGUGCUUU**U*sU*sU*s**U (SEQ ID NO: 115)	113
276	CLTA4_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA4mg ON-target	**G*s**CAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU**U*s**U (SEQ ID NO: 116)	113
277	CLTA4_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA4mg ON-target	**G*s**CAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU**U*s**U (SEQ ID NO: 116)	113
278	CLTA4_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA4mg ON-target	**G*s**CAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU**U*s**U (SEQ ID NO: 116)	113
279	CLTA4_5', 3'-1x(2'OMe, 3'thioPACE)	CLTA4mg OFF5-target	**G*s**CAGAUGUAGUGUUUCCACAGUUUAAGAGCUAUGCUGGAAACAGCAUAG CAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAG UCGGUGCUUUUU**U*s**U (SEQ ID NO: 116)	113
		2-aminoA-modified sgRNA (including unmodified controls)		
280	EN1	EN1mg ON-target	GAUGUUGUCGAUGAAAAAGUGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 117)	113
281	EN1	EN1mg OFF-target	GAUGUUGUCGAUGAAAAAGUGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 117)	113
282	EN1_2aminoA + 16	EN1mg ON-target	GAUGUUGUCGAUGAA(**2aA**)AAGUGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 118)	113
283	EN1_2aminoA + 16	EN1mg OFF-target	GAUGUUGUCGAUGAA(**2aA**)AAGUGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 118)	113
284	PCDHA4	PCDHA4mg ON-target	GAUUUAGACGAAGGAUUGAAGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 119)	113
285	PCDHA4	PCDHA4mg OFF-target	GAUUUAGACGAAGGAUUGAAGUUUAAGAGCUAUGCUGGUAACAGCAUAGC AAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGU CGGUGCUUUUUUU (SEQ ID NO: 119)	113
286	PCDHA4_2aminoA + 15	PCDHA4mg ON-target	GAUUUAGACGAAGG(**2aA**)UUGAAGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 120)	113
287	PCDHA4_2aminoA + 15	PCDHA4mg OFF-target	GAUUUAGACGAAGG(**2aA**)UUGAAGUUUAAGAGCUAUGCUGGUAACAGCAU AGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCG AGUCGGUGCUUUUUUU (SEQ ID NO: 120)	113

TABLE 3-continued

Entry #	Guide RNA Construct	Target DNA Construct	RNA sequence (5'→3')	RNA length
			5-methylU-modified sgRNA	
288	CLTA4_21x(5-MeU)	CLTA4mg ON-target	GCAGA(**5mU**)G(**5mU**)AG(**5mU**)G(**5mU**)(**5mU**)(**5mU**)CCACAGUUUAAGAGC (**5mU**)A(**5mU**)GC(**5mU**)GG(**5mU**)AACAGCA(**5mU**)AGCAAGUUUAAAUAAGG CUAGUCCGUUAUCAAC(**5mU**)(**5mU**)GAAAAAG(**5mU**)GGCACCGAGUCGG (**5mU**)GC(**5mU**)(**5mU**)(**5mU**)(**5mU**)(**5mU**)(**5mU**)U (SEQ ID NO: 121)	113
289	CLTA4_21x(5-MeU)	CLTA4mg OFF5-target	GCAGA(**5mU**)G(**5mU**)AG(**5mU**)G(**5mU**)(**5mU**)(**5mU**)CCACAGUUUAAGAGC (**5mU**)A(**5mU**)GC(**5mU**)GG(**5mU**)AACAGCA(**5mU**)AGCAAGUUUAAAUAAGG CUAGUCCGUUAUCAAC(**5mU**)(**5mU**)GAAAAAG(**5mU**)GGCACCGAGUCGG (**5mU**)GC(**5mU**)(**5mU**)(**5mU**)(**5mU**)(**5mU**)(**5mU**)U (SEQ ID NO: 121)	113
			Z base-modified sgRNA	
290	CLTA1_22_70,71	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGU**ZZ**GUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCUUUUUUU (SEQ ID NO: 122)	113
291	CLTA1 22_95,96	CLTA1 ON1-target	AGUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAGCA AGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCA**ZZ**GAGUC GGUGCUUUUUUU (SEQ ID NO: 122)	113
			sgRNA modified to disfavor misfolding	
292	CLTA1_opti_short_5', 3'-1x(2'OMe, 3'thioPACE)_2'OMe_54,57	CLTA1mg ON1-target	**A*s**GUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAGUAAUAGCAAGUUUAAA UAAGGU**UA**UCCGUUAUCAACAAGAAAUUGUGGCACCGAGUCGGUGCUU**U** ***s***U (SEQ ID NO: 123)	100
293	CLTA1_opti_short_ 5', 3'-1x(2'OMe, 3'thioPACE)_2'OMe_64,67	CLTA1mg ON1-target	**A*s**GUCCUCAUCUCCCUCAAGCGUUUAAGAGCUAUGCUGGUAACAGCAUAG CAAGUUUAAAUAAGG**U**UA**A**UCCGUUAUCAACAAGAAAUUGUGGCACCGAG UCGGUGCUUUUU**U*s**U (SEQ ID NO: 124)	113

N = 2'OMe
N = 2'deoxy
Ns = 3'P(S)
N* = 3'-PACE
N*s = 3'-thioPACE
N* = 2'OMe, 3'-PACE
N*s = 2'OMe, 3'-thioPACE
Ns = 2'OMe, 3'P(S)
N_o = 5'-overhang (5' to the 20-nt guide sequence); "NC" means the overhang is not complementary to protospacer-adjacent sequence
(2sU) = 2-thioU
(2aA) = 2-aminoA
(5mU) = 5-methylU
Z = Z base
IntFl = Fluorophore incorporated at an internal position in the RNA sequence

The DNA target constructs in Table 3 had the following sequences:

CLTA1 ON1-target:	AGAATTTAACTGTGGTCACATTTGCTTTATCGACTGGCTTCATCTCACAGCTCATC TTACGCAAGTTCGATGAGTATGCCAGTCACTTTCAATTTGGTTGAATGTTCCCGTG ACATGCGAGTTCTGTCGACCATGTGCCGCGGATTGAATTCCTCAAGGGTGGTGATA GATGCTACGGTGGTGATGCGCATGCGCTCAGTCCTCATCTCCCTCAAGCAGGCCCC GCTGGTGGGTCGGAGTCCCTAGTGAAGCCACCAATATAGTGGTCGTGTCAAGCAAC TGTCCACGCTCCACCCTCGAGGTCGTAACATAAACGTACTAAGGCACGAGTAAACA AGATCGATAGCAAGAACATGGTATAGACTGACGGAGAGCTCGCCATTAGTCTGA (SEQ ID NO: 10)
CLTA1 OFF1-target:	AGAATTTAACTGTGGTCACATTTGCTTTATCGACTGGCTTCATCTCACAGCTCATC TTACGCAAGTTCGATGAGTATGCCAGTCACTTTCAATTTGGTTGAATGTTCCCGTG ACATGCGAGTTCTGTCGACCATGTGCCGCGGATTGAATTCCTCAAGGGTGGTGATA GATGCTACGGTGGTGATGCGTATGCACTCAGTCCTCAACTCCCTCAAGCAGGCGAC CCCTGGGGGTCGGAGTCCCTAGTGAAGCCACCAATATAGTGGTCGTGTCAAGCAAC TGTCCACGCTCCACCCTCGAGGTCGTAACATAAACGTACTAAGGCACGAGTAAACA AGATCGATAGCAAGAACATGGTATAGACTGACGGAGAGCTCGCCATTAGTCTGA (SEQ ID NO: 11)
CLTA1 OFF2-target:	AGAATTTAACTGTGGTCACATTTGCTTTATCGACTGGCTTCATCTCACAGCTCATC TTACGCAAGTTCGATGAGTATGCCAGTCACTTTCAATTTGGTTGAATGTTCCCGTG ACATGCGAGTTCTGTCGACCATGTGCCGCGGATTGAATTCCTCAAGGGTGGTGATA GATGCTACGGTGGTGATGCAATAAATTTCAGCCCTCATTTCCCTCAAGCAGGGGTT ACTTTAGGGTCGGAGTCCCTAGTGAAGCCACCAATATAGTGGTCGTGTCAAGCAAC TGTCCACGCTCCACCCTCGAGGTCGTAACATAAACGTACTAAGGCACGAGTAAACA AGATCGATAGCAAGAACATGGTATAGACTGACGGAGAGCTCGCCATTAGTCTGA (SEQ ID NO: 12)
CLTA1 OFF3-target:	AGAATTTAACTGTGGTCACATTTGCTTTATCGACTGGCTTCATCTCACAGCTCATC TTACGCAAGTTCGATGAGTATGCCAGTCACTTTCAATTTGGTTGAATGTTCCCGTG ACATGCGAGTTCTGTCGACCATGTGCCGCGGATTGAATTCCTCAAGGGTGGTGATA GATGCTACGGTGGTGATGCTCTCCAGCCCACTCCTCATCCCCCTCAAGCCGGTCCC AGGCTGGGGTCGGAGTCCCTAGTGAAGCCACCAATATAGTGGTCGTGTCAAGCAAC TGTCCACGCTCCACCCTCGAGGTCGTAACATAAACGTACTAAGGCACGAGTAAACA AGATCGATAGCAAGAACATGGTATAGACTGACGGAGAGCTCGCCATTAGTCTGA (SEQ ID NO: 13)
CLTA1mg ON1-target:	GCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGG GCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCAT TTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATA AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTAAATTGTAAGCG TTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAC CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGG GTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCA ACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCA CCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAA AGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGG AAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACG CTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCA TTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGC TATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACG CCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAGCGCGCGTAATA CGACTCACTATAGGGCGAATTGGGTACGATCGATGCGGCCTCGCAGGCCAAAGATG TCTCCCGCATGCGCTCAGTCCTCATCTCCCTCAAGCAGGCCCTGCTGGTGCACTGA AGAGCCACCCTGTGCGCGTGATATGCAGCTCCAGCTTTTGTTCCCTTTAGTGAGGG TTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGG GTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAG AGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCT CGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTA TCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAA GGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC CTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCC GACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAG TGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAA GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA AAACTCACGTTAAGGGATTTTGGTCATGAGATTNTCAAAAAGGATCTTCACCTAGA TCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACT TGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCT ATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGG AGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCG

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GCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG
TCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAG
TAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATC
GTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATC
AAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTC
CTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCA
GCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGG
TGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTT
GCCCGGCGTCAATACGGGATAATACCGCGCCACATAGC
(SEQ ID NO: 14)

CLTA1mg OFF1-target: GCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGG
GCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCAT
TTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATA
AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTAAATTGTAAGCG
TTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAC
CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGG
GTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCA
ACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCA
CCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAA
AGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGG
AAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACG
CTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCA
TTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGC
TATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACG
CCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAGCGCGCGTAATA
CGACTCACTATAGGGCGAATTGGGTACGATCGATGCGGCCTCGCAGGGCAAAGAGG
TCTCCTGTATGCACTCAGTCCTCAACTCCCTCAAGCAGGCGACCCTTGGTGCACTG
ACAAACCGCTCCTGCGCGTGATATGCAGCTCCAGCTTTTGTTCCCTTTAGTGAGGG
TTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA
TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGG
GTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC
CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAG
AGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCT
CGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTA
TCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAA
GGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
CTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCC
GACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC
TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG
CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA
CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA
CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAG
TGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA
CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAA
GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA
AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGA
TCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACT
TGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCT
ATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGG
AGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCG
GCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG
TCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAG
TAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATC
GTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATC
AAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTC
CTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCA
GCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGG
TGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTT
GCCCGGCGTCAATACGGGATAATACCGCGCCACATAGC
(SEQ ID NO: 15)

CLTA1mg_OFF3 target: GCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGG
GCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCAT
TTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATA
AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTAAATTGTAAGCG
TTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAC
CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGG
GTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCA
ACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCA
CCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAA
AGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGG
AAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACG
CTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCCCA
TTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGC
TATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACG
CCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAGCGCGCGTAATA

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	CGACTCACTATAGGGCGAATTGGGTACGATCGATGCGGCCTCAGGAGAGGGAGCCA
	TGCTCATCTCCAGCCCACTCCTCATCCCCCTCAAGCCGGTCCCAGGCTGAGAGGCT
	AAAGCTTGTCTTTGCGCGTGATATGCAGCTCCAGCTTTTGTTCCCTTTAGTGAGGG
	TTAATTGCGCGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA
	TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGG
	GTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC
	CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAG
	AGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCT
	CGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTA
	TCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAA
	GGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
	CTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA
	CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCC
	GACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC
	TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG
	CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA
	CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA
	CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAG
	TGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
	GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA
	CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAA
	GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA
	AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGA
	TCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACT
	TGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCT
	ATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGG
	AGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCG
	GCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG
	TCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAG
	TAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATC
	GTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATC
	AAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTC
	CTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCA
	GCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGG
	TGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTT
	GCCCGGCGTCAATACGGGATAATACCGCGCCACATAGC
	(SEQ ID NO: 16)
CLTA4 ON-target:	GCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGA
	GTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTAT
	GCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACG
	ATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAAC
	TCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTG
	ACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAA
	CTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGT
	TGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAAT
	CTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGT
	AAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGA
	ACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGT
	CAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTT
	AAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACG
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	(SEQ ID NO: 17)
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	(SEQ ID NO: 18)
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(SEQ ID NO: 19)

IL2RGmg_ON target: GCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGG
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(SEQ ID NO: 20)

EN1mg_ON target:
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(SEQ ID NO: 21)

EN1mg_OFF target:
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GCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGG
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(SEQ ID NO: 22)

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CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA
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GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA
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	GCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG
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	TAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATC
	GTGGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATC
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	CTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCA
	GCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGG
	TGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTT
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	(SEQ ID NO: 23)
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	AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTAAATTGTAAGCG
	TTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAC
	CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGG
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	AGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGG
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	TCATCCCAATGCCTCAGATTTAGACGAAGGCTTGAATGGGGATATTATTTACTCCT
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	AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGA
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	GCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG
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	CTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCA
	GCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGG
	TGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTT
	CCCGGCGTCAATACGGGATAATACCGCGCCACATAGC
	(SEQ ID NO: 24)

In a 20-uL reaction volume, 50 fmoles of linearized DNA target in the presence of 50 nM sgRNA, 39 nM recombinant purified Cas9 protein (*S. pyogenes*; Agilent) and 10 mM or 0.8 mM $MgCl_2$ at pH 7.6 was incubated at 37° C. for 30 min. Upon completion, 0.5 uL of RNace It (Agilent) was added, and incubation was continued at 37° C. for 5 min and then at 70° C. for 15 min. Subsequently 0.5 μL of Proteinase K (Mol. Bio. grade, NEB) was added and incubated at 37° C. for 15 min. Aliquots were loaded into a DNA 1000 or DNA 7500 LabChip and were analyzed on a Bioanalyzer 2200, or alternatively were loaded into a Genomic DNA ScreenTape and were analyzed on a TapeStation. The workup steps served to release Cas9 from binding of target DNA, which was assayed for cleavage. Cleavage yields were calculated

by the formula: a/(a+b)×100 where a is the sum of the band intensities of the two cleavage products and b is the remaining uncleaved DNA if present. A cleavage percentage of 100% means that all of the target DNA construct was cleaved.

A series of guide RNAs were chemically synthesized. The guide RNA oligomers were synthesized on an ABI 394 Synthesizer (Life Technologies, Carlsbad, Calif., USA) using 2'-O-thionocarbamate-protected nucleoside phosphoramidites according to procedures described in Dellinger et al. (2011) *J. Am. Chem. Soc.*, 133, 11540-56. 2'-O-methyl phosphoramidites were incorporated into RNA oligomers under the same conditions as the 2'-O-thionocarbamate protected phosphoramidites. The 2'-O-methyl-3-O-(diisopropylamino)phosphinoacetic acid-1,1-dimethylcyanoethyl ester-5'-O-dimethoxytrityl nucleosides used for synthesis of thiophosphonoacetate (thioPACE)-modified RNAs were synthesized essentially according to published methods. See Dellinger et al. (2003) 1 Am. Chem. Soc., 125, 940-50; and Threlfall et al. (2012) *Org. Biomol. Chem.*, 10, 746-54. For phosphorothioate-containing oligomers, the iodine oxidation step after the coupling reaction was replaced by a sulfurization step using a 0.05 M solution of 3-((N,N-dimethylaminomethylidene)amino)-3H-1,2,4-dithiazole-5-thione in a pyridine-acetonitrile (3:2) mixture for 6 min.

All the oligonucleotides were purified using reversed-phase high-performance liquid chromatography (HPLC) and analyzed by liquid chromatography-mass spectrometry (LC-MS) using an Agilent 1290 Infinity series LC system coupled to an Agilent 6520 Q-TOF (time-of-flight) mass spectrometer (Agilent Technologies, Santa Clara, Calif., USA). The yields for the synthesis and purification of the sgRNAs were estimated using deconvolution of mass spectra obtained from LC-MS-derived total ion chromatograms. The chemical synthesis of the 100-mer sgRNAs typically yielded 25-35% full-length product from a nominal 1 micromole scale synthesis. Reversed-phase HPLC purification using ion pairing buffer conditions typically gave 20% yield from the crude product with an estimated purity of the final sgRNA in the range of 90% to 95%.

The results are shown in Table 4. "% Target cleaved" indicates the percentage of the target DNA construct which was cleaved. Experiments were run with and without addition of a molar excess of targetless competitor DNA (tcDNA) which potentially competes with the target DNA, so the potential impact of the added nonspecific DNA upon the assay could be seen.

TABLE 4

Entry #	[Mg^{2+}] (mM)	tcDNA	% Target cleaved	% CV	% Cleaved vs. CONTROL	% CV CONTROL
2-piece dual-guide scaffold Unmodified dual-guide RNA (dgRNA)						
1	0.8	N	99%	—		
2	0.8	Y	99%	5%		
3	0.8	N	96%	—		
4	0.8	Y	100%	5%		
5	0.8	N	96%	—		
6	0.8	Y	0%	5%		
7	0.8	N	99%	—		
8	0.8	Y	100%	5%		
9	10	N	94%, 93%	—		
10	0.8	Y	88%	—		
Fluorophore-coupled dgRNA						
11	10	N	92%, 93%	—	94%, 93%	—
2'OMethyl-modified dgRNA						
12	0.8	Y	87%	—	88%	—

TABLE 4-continued

Entry #	[Mg^{2+}] (mM)	tcDNA	% Target cleaved	% CV	% Cleaved vs. CONTROL	% CV CONTROL
2'OMethyl,3'Phosphorothioate-modified dgRNA						
13	0.8	Y	87%	—	88%	—
2'OMethyl,3'PhosphorothioPACE-modified dgRNA						
14	0.8	Y	89%	—	88%	—
15	0.8	Y	86%	—	88%	—
2-thioU-modified dgRNA						
16	0.8	N	96%	—	99%	—
17	0.8	Y	95%	5%	99%	5%
18	0.8	N	95%	—	96%	—
19	0.8	Y	100%	5%	100%	5%
20	0.8	N	97%	—	96%	—
21	0.8	Y	0%	5%	0%	5%
22	0.8	N	98%	—	99%	—
23	0.8	Y	99%	5%	100%	5%
24	0.8	N	94%	—	99%	—
25	0.8	Y	83%	5%	99%	5%
26	0.8	N	93%	—	96%	—
27	0.8	Y	94%	5%	100%	5%
28	0.8	N	90%	—	96%	—
29	0.8	Y	0%	5%	0%	5%
30	0.8	N	95%	—	99%	—
31	0.8	Y	94%	5%	100%	5%
32	0.8	N	92%	—	99%	—
33	0.8	Y	84%	5%	99%	5%
34	0.8	N	90%	—	96%	—
35	0.8	Y	94%	5%	100%	5%
36	0.8	N	70%	—	96%	—
37	0.8	Y	0%	5%	0%	5%
38	0.8	N	96%	—	99%	—
39	0.8	Y	59%	5%	100%	5%
Single-guide scaffold Unmodified single-guide RNA (sgRNA)						
40	10	N	93%	—		
41	10	N	94%	—		
42	10	N	94%	—		
43	10	N	92%	—		
44	10	N	90%, 92%	—		
45	10	N	92%	—		
46	10	N	93%	—		
47	0.8	N	86%	—		
48	0.8	N	87%	—		
49	0.8	Y	87%	—		
50	0.8	N	82%	—		
51	0.8	N	92%	—		
52	10	N	60%	—		
53	0.8	N	90%	—		
54	0.8	N	90%	—		
55	0.8	Y	79%	—		
56	0.8	N	79%	—		
57	0.8	N	94%	—		
58	10	N	73%	—		
59	0.8	N	84%	—		
60	0.8	Y	≥85%	—		
61	0.8	Y	89%	—		
62	0.8	N	87%, 82%	—		
63	0.8	N	23%, 22%	—		
64	0.8	N	78%	—	87%	—
65	0.8	Y	76%	—	87%	—
66	0.8	N	65%	—	87%	—
67	0.8	N	81%	—	87%	—
68	0.8	N	85%	—	87%	—
69	0.8	Y	71%	—	87%	—
70	0.8	N	32%	—	87%	—
71	0.8	N	84%	—	87%	—
72	0.8	N	91%	—	87%	—
73	0.8	Y	79%	—	87%	—
74	0.8	N	88%	—	87%	—
75	0.8	N	93%	—	87%	—
76	0.8	N	87%	—	87%	—
77	0.8	Y	79%	—	87%	—
78	0.8	N	89%	—	87%	—
79	0.8	N	88%	—	87%	—
80	0.8	N	3%	—	86%	—

TABLE 4-continued

Entry #	[Mg^{2+}] (mM)	tcDNA	% Target cleaved	% CV	% Cleaved vs. CONTROL	% CV CONTROL
81	0.8	N	5%	—	86%	—
82	0.8	N	89%	—	86%	—
83	0.8	N	68%	—	87%	—
84	0.8	Y	50%	—	87%	—
85	0.8	N	69%	—	87%	—
86	0.8	N	69%	—	87%	—
87	0.8	N	76%	—	87%	—
88	0.8	Y	42%	—	87%	—
89	0.8	N	72%	—	87%	—
90	0.8	N	78%	—	87%	—
91	0.8	N	85%	—	87%	—
92	0.8	Y	51%	—	87%	—
93	0.8	N	82%	—	87%	—
94	0.8	"	83%	—	87%	—
DMT-modified sgRNA						
95	10	N	93%	—	92%	—
96	10	N	93%	—	92%	—
Fluorophore-modified sgRNA						
97	10	N	91%, 91%	—	90%, 92%	—
98	0.8	N	86%	—	87%	—
99	0.8	Y	77%	—	87%	—
100	0.8	N	87%	—	87%	—
101	0.8	N	86%	—	87%	—
102	0.8	N	91%	—	87%	—
103	0.8	Y	82%	—	87%	—
104	0.8	N	90%	—	87%	—
105	0.8	N	92%	—	87%	—
106	0.8	N	91%	—	87%	—
107	0.8	Y	82%	—	87%	—
108	0.8	N	90%	—	87%	—
109	0.8	N	91%	—	87%	—
110	0.8	N	92%	—	87%	—
111	0.8	Y	84%	—	87%	—
112	0.8	N	92%	—	87%	—
113	0.8	N	89%	—	87%	—
114	0.8	N	84%, 84%	—	87%, 82%	—
115	0.8	N	12%, 6%	—	23%, 22%	—
116	0.8	N	93%, 90%	—	87%, 82%	—
117	0.8	N	8%, 9%	—	23%, 22%	—
3'Phosphorothioate-modified sgRNA						
118	10	N	95%	—	90%, 92%	—
119	10	N	94%	—	90%, 92%	—
120	10	N	97%	—	90%, 92%	—
121	10	N	94%	—	90%, 92%	—
2'OMethyl-modified sgRNA						
122	10	N	91%	—	94%	—
123	10	N	92%	—	93%	—
124	0.8	N	86%	—	87%	—
125	"	Y	77%	—	87%	—
126	"	N	85%	—	87%	—
127	0.8	N	88%	—	87%	—
128	10	N	92%	—	94%	—
129	0.8	N	83%	—	87%	—
130	0.8	Y	78%	—	87%	—
131	0.8	N	83%	—	87%	—
132	0.8	N	85%	—	87%	—
133	10	N	92%	—	94%	—
134	0.8	N	86%	—	87%	—
135	0.8	Y	78%	—	87%	—
136	0.8	N	83%	—	87%	—
137	0.8	N	88%	—	87%	—
138	10	N	91%	—	94%	—
139	0.8	N	84%	—	87%	—
140	0.8	Y	81%	—	87%	—
141	0.8	N	83%	—	87%	—
142	0.8	N	87%	—	87%	—
143	10	N	89%	—	92%	—
144	0.8	N	91%, 88%	—	87%, 82%	—
145	0.8	N	24%, 25%	—	23%, 22%	—
146	10	N	93%, 92%	—	90%, 92%	—
147	0.8	N	22%	—	87%	—
148	0.8	Y	3%	—	87%	—
149	0.8	N	12%	—	87%	—

TABLE 4-continued

Entry #	[Mg^{2+}] (mM)	tcDNA	% Target cleaved	% CV	% Cleaved vs. CONTROL	% CV CONTROL
150	0.8	N	5%	—	87%	—
151	10	N	0%, 0%	—	90%, 92%	—
152	10	N	0%, 0%	—	90%, 92%	—
153	0.8	N	85%	—	86%	—
154	0.8	N	87%	—	86%	—
155	0.8	N	89%	—	87%	—
156	0.8	Y	78%	—	87%	—
157	0.8	N	84%	—	87%	—
158	0.8	N	93%	—	87%	—
159	0.8	N	90%	—	86%	—
160	0.8	N	90%	—	87%	—
161	0.8	Y	86%	—	87%	—
162	0.8	N	90%	—	87%	—
163	0.8	N	91%	—	87%	—
164	0.8	N	92%	—	90%	—
165	0.8	N	89%	—	87%	—
166	0.8	Y	80%	—	87%	—
167	0.8	N	90%	—	87%	—
168	0.8	N	94%	—	87%	—
169	0.8	N	90%	—	84%	—
170	0.8	Y	≥85%	—	≥85%	—
171	0.8	N	7%	—	84%	—
172	0.8	Y	0%	—	≥85%	—
173	10	N	15%	—	73%	—
174	0.8	N	85%	—	84%	—
175	0.8	Y	75%	—	≥85%	—
176	10	N	86%	—	73%	—
177	0.8	"	0%	—	84%	—
178	0.8	Y	0%	—	≥85%	—
179	10	N	15%	—	73%	—
2'Deoxy-modified sgRNA						
180	10	N	27%, 19%	—	90%, 92%	—
181	10	N	0%, 0%	—	90%, 92%	—
182	10	N	0%, 0%	—	90%, 92%	—
2'Deoxy,3'PACE-modified sgRNA						
183	0.8	N	72%, 77%	—	87%, 82%	—
184	0.8	N	8%, 9%	—	23%, 22%	—
2'OMethyl,3'PACE-modified sgRNA						
185	0.8	N	82%	—	87%	—
186	0.8	Y	72%	—	87%	—
187	10	Y	95%	—	93%	—
188	10	Y	95%	—	94%	—
189	0.8	Y	91%	—	87%	—
190	0.8	Y	84%	—	87%	—
191	0.8	Y	85%	—	87%	—
192	0.8	Y	77%	—	87%	—
193	10	Y	88%	—	94%	—
194	0.8	Y	70%	—	87%	—
195	0.8	Y	56%	—	87%	—
196	0.8	Y	40%	—	87%	—
197	0.8	Y	23%	—	87%	—
198	10	Y	88%	—	93%	—
199	10	Y	89%	—	94%	—
200	0.8	Y	84%	—	87%	—
201	0.8	Y	75%	—	87%	—
202	10	Y	90%	—	93%	—
203	10	Y	90%	—	94%	—
204	0.8	Y	86%	—	87%	—
205	0.8	Y	82%	—	87%	—
206	10	Y	88%	—	93%	—
207	0.8	Y	82%	—	87%	—
208	0.8	Y	78%	—	87%	—
209	10	Y	77%	—	93%	—
210	0.8	Y	71%	—	87%	—
211	"	Y	69%	—	"	—
212	10	N	80%	—	93%	—
213	0.8	N	56%	—	87%	—
214	0.8	Y	41%	—	"	—
215	10	Y	78%	—	93%	—
216	0.8	Y	58%	—	87%	—
217	0.8	Y	44%	—	"	—
218	10	Y	80%	—	93%	—
219	0.8	Y	39%	—	87%	—
220	0.8	Y	13%	—	"	—

TABLE 4-continued

Entry #	[Mg^{2+}] (mM)	tcDNA	% Target cleaved	% CV	% Cleaved vs. CONTROL	% CV CONTROL
221	10	Y	74%	—	93%	—
222	0.8	Y	36%	—	87%	—
223	0.8	Y	19%	—	87%	—
224	10	Y	86%	—	93%	—
225	0.8	Y	84%	—	87%	—
226	0.8	Y	80%	—	"	—
227	10	Y	88%	—	93%	—
228	0.8	Y	83%	—	87%	—
229	0.8	Y	82%	—	87%	—
230	0.8	N	80%	—	87%	—
231	0.8	N	84%	—	87%	—
232	10	N	88%	—	93%	—
233	0.8	N	85%	—	87%	—
234	0.8	Y	73%	—	87%	—
235	10	Y	82%	—	93%	—
236	0.8	Y	89%	—	87%	—
237	0.8	Y	76%	—	87%	—
238	10	Y	65%	—	93%	—
239	0.8	Y	84%	—	87%	—
240	0.8	Y	56%	—	87%	—
2'OMethyl,3'Phosphorothioate-modified sgRNA						
241	10	N	92%	—	92%	—
242	0.8	N	84%	—	87%	—
243	0.8	Y	88%	—	87%	—
244	0.8	N	85%	—	87%	—
245	0.8	N	91%	—	87%	—
246	0.8	N	91%	—	84%	—
247	0.8	Y	≥85%	—	≥85%	—
248	0.8	N	84%	—	84%	—
249	0.8	Y	90%	—	89%	—
250	0.8	N	90%, 87%	—	87%, 82%	—
251	0.8	N	16%, 19%	—	23%, 22%	—
252	0.8	N	93%	—	89%	—
253	0.8	N	90%, 90%	—	87%, 82%	—
254	0.8	N	17%, 22%	—	23%, 22%	—
255	0.8	N	93%	—	89%	—
256	0.8	N	91%, 91%	—	87%, 82%	—
257	0.8	N	13%, 16%	—	23%, 22%	—
2'OMethyl,3'PhosphorothioPACE-modified sgRNA						
258	10	N	89%	—	92%	—
259	0.8	N	84%	—	87%	—
260	0.8	Y	80%	—	87%	—
261	0.8	N	77%	—	87%	—
262	0.8	N	83%	—	87%	—
263	0.8	N	92%	—	87%	—
264	0.8	Y	79%	—	87%	—
265	0.8	N	88%	—	87%	—
266	0.8	N	94%	—	87%	—
267	10	N	74%	—	93%	—
268	0.8	N	11%	—	86%	—
269	0.8	N	15%	—	"	—
270	0.8	N	49%	—	"	—
271	0.8	N	31%	—	"	—
272	0.8	N	91%	—	84%	—
273	0.8	Y	77%	—	≥85%	—
274	0.8	N	90%, 91%	—	87%, 82%	—
275	0.8	N	9%, 8%	—	23%, 22%	—
276	0.8	N	90%	—	84%	—
277	0.8	Y	≥85%	—	≥85%	—
278	0.8	N	86%, 88%	—	87%, 82%	—
279	0.8	N	11%, 7%	—	23%, 22%	—
2-aminoA-modified sgRNA (including unmodified controls)						
280	0.8	Y	88%, 88%	—		
281	0.8	Y	76%, 75%	—		
282	0.8	Y	87%, 91%	—	88%, 88%	—
283	0.8	Y	90%, 90%	—	76%, 75%	—
284	0.8	Y	85%, 87%	—		
285	0.8	Y	88%, 88%	—		
286	0.8	Y	93%, 96%	—	85%, 87%	—
287	0.8	Y	82%, 79%	—	88%, 88%	—
5-methylU-modified sgRNA						
288	0.8	N	86%, 83%	—	87%, 82%	—
289	0.8	N	11%, 11%	—	23%, 22%	—

TABLE 4-continued

Entry #	[Mg^{2+}] (mM)	tcDNA	% Target cleaved	% CV	% Cleaved vs. CONTROL	% CV CONTROL
Z base-modified sgRNA						
290	10	N	19%	—	92%	—
291	10	N	93%	—	"	—
sgRNA modified to disfavor misfolding						
292	0.8	N	93%	—	90%	—
293	0.8	N	93%	—	86%	—

The results revealed that guide RNAs containing modifications at specific positions were tolerated by active Cas protein and gRNA:Cas protein complexes, as the modifications did not prevent target-specific cleavage of the on-target polynucleotide. The modifications that were tested and found to be tolerated at specific positions include 2'-O-methylribonucleotide (=2'OMe), 2'-deoxyribonucleotide, racemic phosphorothioate internucleotide linkage, 3'-phosphonoacetate (=PACE), 3'-thiophosphonoacetate (=thioPACE), Z nucleotide, 2-thiouracil, 2-aminoadenine, 5-methyluracil, 5-aminoallyluracil coupled to Cy5 fluorophore, 2-(4-butylamidofluorescein)propane-1,3-diol bis (phosphodiester) linker, and combinations of these.

It is contemplated that the chemical modifications disclosed and tested herein, particularly at the tested positions (as listed in Tables 3 and 4), will be tolerated at equivalent positions in a variety of guide RNAs.

As disclosed herein, chemically modified nucleotides were incorporated into guide RNAs in an effort to improve certain properties. Such properties include improved nuclease resistance of the guide RNA (also known as improved stability), reduced off-target effects of a gRNA:Cas protein complex (also known as improved specificity), improved efficacy of gRNA:Cas protein complex when cleaving, nicking or binding a target polynucleotide, improved transfection efficiency, and/or improved organelle localization.

The assay results in Tables 3 and 4 indicate that: (1) In guide RNAs, many positions can tolerate a variety of chemical modifications; (2) 5' and 3' ends of guide RNAs will tolerate a wide variety of end-protecting modifications, and such modifications are useful to inhibit exonucleolytic RNA degradation; (3) 2-ThioU can be used to deter off-target interactions involving G-U wobble pairings, thereby increasing the specificity of guide pairing by inhibiting off-target hybridization interactions; (4) 5' Extensions are generally well-tolerated; (5) Surface exposed regions of the guide RNA (as inferred from published crystal structures) are tolerant of extensively modifying U's to 5-methylU's, which potentially make the modified RNA more likely to elude immune responses such as stimulated by unmodified RNA; and (6) For RNA folding, G-C pairs are stronger and more stable than A-U pairs. At least one guide RNA is tolerant of replacing some G-C pairs with 2'-O-methylA-2'-O-methylU pairs that are more stable thermodynamically than unmodified A-U pairs.

More particularly, the present example shows that 2'-O-methyl modifications are tolerated at the 5' and 3' ends of dual-guide RNAs (as shown by entry 12 in Tables 3 and 4) and single-guide RNAs (entries 143-146, 169-170), thus allowing end-protection to stabilize gRNAs against exonucleases. 2'-O-methyl modifications are tolerated at most but not all internal positions, thus allowing stabilization against various nucleases including endonucleases (entries 146, 153-168, 174-179). However, the present example also

demonstrates that not every position in guide RNAs will tolerate 2'-O-methyls (as shown by entries 151-152 and 171-173), suggesting that too many consecutive 2'-O-methyl modifications at the 5' end (e.g., 26 or more consecutive 2'-O-methyl-modified nucleotides), or too many 2'-O-methyl modifications of C and U nucleotides downstream (3') of the 5'-terminal 20mer guide sequence is not well tolerated (e.g., the inhibitory effect of one or both 2'-O-methyluracils at sequence positions +56 and +69 in entries 171-173 as revealed by the positions tested in entries 154-156).

The present example shows that 2'-O-methyl modifications throughout the 20mer guide sequence are tolerated during in vitro uses in buffer containing 10 mM Mg^{2+} (entry 146), but such extensive modification is not well tolerated under physiological conditions (entries 147-150) as present in cells. Thus, in some embodiments, a gRNA comprising 15 or more, alternatively 17 or more, alternatively 18 or more, alternatively 20 2'-O-methyl modifications throughout the 20mer guide sequence is used for in vitro methods as described herein, such as genomic editing to modify a DNA sequence in vitro, regulating the expression of a gene of interest in vitro, cleaving a DNA target sequence in vitro, and other uses.

The present example shows that extensive incorporation of 2'-deoxy modifications is not well tolerated and can be substantially completely inhibitory (entries 180-182). However, 2'-deoxy modifications can be well-tolerated at some locations (entry 183), therefore such modification can be useful for inhibiting nucleases.

The present example also shows that fluorophore or dye labels are tolerated in every loop of the three known stem-loops in CRISPR-Cas9 guide RNAs (entry 116). Such labels are also tolerated in a 5' overhang on the guide sequence (entry 114), tolerated at additional locations in sgRNAs (entry 114), and tolerated in a loop in tracrRNA used in dual-guide applications (entry 11). In this example, two different types of fluorophores were tested: a phosphodiester-linked fluorophore (no ribose ring) that essentially takes the place of a nucleotide (entries 114 & 116), and a dye label (Cy5) covalently coupled to 5-aminoallylU incorporated in a guide RNA (entry 11).

The present example also shows that Z bases are tolerated in synthetic guide RNAs, particularly as modifications of synthetic guide RNAs in which some C's are replaced with Z bases (entries 290-291). The present example also shows that several other bases are tolerated at various positions, as shown in Tables 3 and 4.

The present example further shows that the 5' and 3' ends of guide RNAs can tolerate a wide variety of end-protecting modifications. Such modifications can be used to inhibit exonucleolytic RNA degradation. Support for the tolerance of such modifications can be found in Hendel et al., *Nat. Biotechnol.* (2015) 33:9, 985-9. Additional support for modifications at the 5' and 3' ends of guide RNAs is provided by entries 143-144, 185-223, 241-257, 258-266, and 272-279 in Tables 3 and 4. In some embodiments, the guide RNA comprises 7 or fewer modified nucleotides at a 5' end or a 3' end or at each of 5' and 3' ends, alternatively 6 or fewer, alternatively 5 or fewer, alternatively 4 or fewer, alternatively 3 or fewer, alternatively 2 or fewer, alternatively 1. Dual-guide RNAs can be protected similarly (entries 12-15).

The present example further shows that 2-thioU can be used to deter off-target interactions involving G-U wobble pairings, thereby increasing the specificity of guide sequence pairing by inhibiting off-target hybridization interactions (entries 16-39). One of the base pairs involved in hybridization between the guide RNA and CLTA1 OFF-target 3 (also referred to as "CLTA1 OFF3-target" or "CLTA1 OFF3") is a G-U wobble pair. Replacing the corresponding U in the guide RNA with a 2-thioU reduces cleavage from 100% (entry 8) to 59% (entry 39). Replacing other U's with 2-thioU's (e.g., at sequence position +3 or +9, entries 23 and 31) does not have the same effect, presumably because those U's do not involve G-U wobble pairing when fully hybridized to each of the OFF-target sites tested. Accordingly, 2-thioU can increase target specificity of guide RNAs when off-target sites involve G-U wobble pairing.

The present example also shows that 5'-overhang sequences attached to the guide sequence are generally well-tolerated (see entries 83-95, 114, and 206-223). For example, a bulky dimethoxytrityl (dmt) group at the 5' end was well tolerated (entry 95). The chromatographic properties of dmt can be used to facilitate purification of full-length synthetic RNAs from incompletely elongated byproducts which are generally produced during synthesis. Accordingly, in some embodiments, the synthetic guide RNA comprises a 5'-overhang sequence, for example, comprising a short polynucleotide sequence of 15 or fewer nucleotides which is complementary to the guide sequence and is covalently linked at its 3' end to the 5' end of the guide sequence by a polymeric linker such as a polynucleotide or similarphosphodiester-based linker, in which the linker can be 5 or more consecutive uridine nucleotides, alternatively 6 or 7.

The present example also shows that surface exposed regions of the guide RNA (as inferred from crystal structures published by others) are tolerant of extensively modifying uracils nucleotides to 5-methyluracils (5-methylU's) (entry 288), which can make the modified RNA more likely to elude immune responses such as stimulated by unmodified RNA. In particular, the 5' and 3' ends of a synthetic guide RNA are potentially immunostimulatory, and the present example shows that 5' and 3' ends are tolerant of 5-methylU modifications (entry 288).

The present example also shows that a synthetic guide RNA is tolerant of replacing some G-C pairs with 2'-O-methylA-2'-O-methylU pairs which are more stable thermodynamically than unmodified A-U pairs (see the non-terminal-2'-O-methylU and complementary-2'-O-methylA modifications in entries 292-293). This is advantageous because it is known that, for folded RNAs, G-C pairs are stronger and more stable than A-U pairs. Replacement of G-C pairs with such thermostabilized A-U pairs in synthetic guide RNAs allows for improved folding of active structures by preventing misfolded structures that involve unintended G-C pair(s), as can be predicted by RNA folding algorithms in common use.

EXEMPLARY EMBODIMENTS

Exemplary embodiments provided in accordance with the presently disclosed subject matter include, but are not limited to, the claims and the following embodiments:

A1. A synthetic guide RNA comprising:

a crRNA segment comprising (i) a guide sequence capable of hybridizing to a target sequence, (ii) a stem sequence; and

a tracrRNA segment comprising a nucleotide sequence that is partially or completely complementary to the stem sequence, wherein the synthetic guide RNA comprises at least one modified nucleotide, and wherein the synthetic guide RNA has gRNA functionality.

A2. The synthetic guide RNA of embodiment A1, comprising a 2'-deoxy moiety.

A3. The synthetic guide RNA of embodiment A1 or A2, comprising a 2'-halo moiety selected from 2'-fluoro, 2'-chloro, 2'-bromo and 2'-iodo.

A4. The synthetic guide RNA of any one of the preceding embodiments, comprising a phosphorothioate group.

A5. The synthetic guide RNA of any one of the preceding embodiments, comprising a PACE group.

A6. The synthetic guide RNA of any one of the preceding embodiments, comprising a thioPACE group.

A7. The synthetic guide RNA of any one of embodiments A2-A6, comprising a 2'-O-methyl moiety.

A8. The synthetic guide RNA of any one of the preceding embodiments, comprising a 2-thiouracil.

A9. The synthetic guide RNA of any one of the preceding embodiments, comprising a 4-thiouracil.

A10. The synthetic guide RNA of any one of the preceding embodiments, comprising a 2-aminoadenine.

A11. The synthetic guide RNA of any one of the preceding embodiments, comprising a hypoxanthine.

A12. The synthetic guide RNA of any one of the preceding embodiments, comprising a 5-methylcytosine.

A13. The synthetic guide RNA of any one of the preceding embodiments, comprising a 5-methyluracil.

A14. The synthetic guide RNA of any one of the preceding embodiments, comprising a 5-aminoallyl-uracil.

A15. The synthetic guide RNA of any one of the preceding embodiments, comprising a Z ribonucleotide.

A16. The synthetic guide RNA of any one of the preceding embodiments, comprising a Z deoxyribonucleotide.

A17. The synthetic guide RNA of any one of the preceding embodiments, comprising a squarate conjugation.

A18. The synthetic guide RNA of any one of the preceding embodiments, comprising a dye linker.

A19. The synthetic guide RNA of embodiment A18, wherein the dye linker is 2-(4-butylamidofluorescein)propane-1,3-diol bis(phosphodiester) linker.

A20. The synthetic guide RNA of any one of the preceding embodiments, comprising a nucleotide with 2'-O-methyl and 3'-phosphorothioate.

A21. The synthetic guide RNA of any one of the preceding embodiments, comprising a nucleotide with 2'-O-methyl and 3"-PACE.

A22. The synthetic guide RNA of any one of the preceding embodiments, comprising a nucleotide with 2'-O-methyl and 3'-thioPACE.

A23. The synthetic guide RNA of any one of the preceding embodiments, comprising a nucleotide with 2'-deoxy and 3'-PACE.

A24. The synthetic guide RNA of any one of the preceding embodiments, comprising a 5-methylcytidine.

A25. The synthetic guide RNA of any one of the preceding embodiments, comprising a methylphosphonate.

A26. The synthetic guide RNA of any one of the preceding embodiments, comprising an ester of PACE, wherein the ester is optionally a methyl ester.

A27. The synthetic guide RNA of any one of the preceding embodiments, comprising a a single RNA strand comprising both the cr RNA segment and the tracr RNA segment.

A28. The synthetic guide RNA of any one of embodiments A1-A26, comprising two RNA strands, and the cr RNA segment and the tracr RNA segment are in different RNA strands.

A29. The synthetic guide RNA of any one of the preceding embodiments, comprising a modified nucleotide at a 5' end, 3' end, or both 5' end and 3' end of each RNA strand.

A30. The synthetic guide RNA of any one of the preceding embodiments, comprising a modified nucleotide in the guide sequence.

A31. The synthetic guide RNA of any one of the preceding embodiments, comprising a modified nucleotide 5' to the guide sequence.

A32. The synthetic guide RNA of any one of the preceding embodiments, comprising a modified nucleotide in the stem sequence.

A33. The synthetic guide RNA of any one of the preceding embodiments, comprising a modified nucleotide in the scaffold region.

A34. The synthetic guide RNA of any one of the preceding embodiments, comprising at least one unnatural, orthogonal base pair in the scaffold region, wherein the base pair is independently selected from isoG-isoC and Z base-P base.

A35. The synthetic guide RNA of any one of the preceding embodiments, comprising a 2'-amino group.

A36. The synthetic guide RNA of any one of the preceding embodiments, comprising a phosphorodithioate linkage group.

A37. The synthetic guide RNA of any one of the preceding embodiments, comprising a boranophosphonate linkage group.

A38. The synthetic guide RNA of any one of the preceding embodiments, comprising an unlocked nucleic acid modification (ULNA).

A39. The synthetic guide RNA of any one of the preceding embodiments, comprising a locked nucleic acid modification (LNA).

A40. The synthetic guide RNA of any one of the preceding embodiments, comprising an unstructured nucleic acid modification (UNA).

A41. The synthetic guide RNA of any one of the preceding embodiments, comprising a pseudoU.

A42. The synthetic guide RNA of any one of the preceding embodiments, comprising a 2'-MOE.

A43. The synthetic guide RNA of any one of the preceding embodiments, comprising a 2'-arabino.

A44. The synthetic guide RNA of any one of the preceding embodiments, comprising a 4'-thioribose.

A45. The synthetic guide RNA of any one of the preceding embodiments, comprising a squarate linkage

A46. The synthetic guide RNA of any one of the preceding embodiments, comprising a triazaolo linkage.

A47. A method for cleaving or nicking a target polynucleotide comprising contacting the target polynucleotide with a CRISPR-associated protein and the synthetic guide RNA of any one of the preceding embodiments, and cleaving or nicking the target polynucleotide.

A48. The method of embodiment A47, wherein the cleaving or nicking takes place in vitro.

A49. The method of embodiment A47, wherein the cleaving or nicking takes place in a cell.

A50. The method of embodiment A47, wherein the cleaving or nicking takes place in vivo.

A51. The method of any one of embodiments A47-A50, wherein the CRISPR-associated protein is Cas9.

A52. The method of any one of embodiments A47-A51, wherein the cleaving or nicking results in gene editing.

A53. The method of any one of embodiments A47-A52, wherein the cleaving or nicking results in alteration of gene expression.

A54. A method for binding a target polynucleotide comprising contacting the target polynucleotide with a CRISPR-associated protein and the synthetic guide RNA of any one of the preceding embodiments,

A55. The method of embodiment A54, wherein the CRISPR-associated protein comprises a mutant which does not have a cleavage or nicking activity.

A56. The method of embodiment A54 or A55, wherein the the CRISPR-associated protein is a fusion protein comprising a protein component not naturally existing in a CRISPR system.

A57. The method of any one of embodiments A54 to A56, resulting in a change of expression of the target polynucleotide.

A58. The method of any one of embodiments A54 to A57 useful to tag the target polynucleotide.

FURTHER EXEMPLARY EMBODIMENTS

B1. A synthetic guide RNA comprising:

(a) a crRNA segment comprising (i) a guide sequence capable of hybridizing to a target sequence in a polynucleotide, (ii) a stem sequence; and

(b) a tracrRNA segment comprising a nucleotide sequence that is partially or completely complementary to the stem sequence, wherein the synthetic guide RNA comprises one or more modifications, and wherein the synthetic guide RNA has gRNA functionality.

B2. The synthetic guide RNA of embodiment 1, comprising a 2'-O-methyl moiety, a 2'-deoxy moiety, a Z base, a phosphorothioate internucleotide linkage, a phosphonoacetate internucleotide linkage, a thiophosphonoacetate internucleotide linkage, or combinations thereof.

B3. The synthetic guide RNA of embodiment 1 or 2, comprising one or more modifications selected from the group consisting of a 2'-O-methyl nucleotide with a 3'-phosphorothioate group, a 2'-O-methyl nucleotide with a 3'-phosphonocarboxylate group, a 2'-O-methyl nucleotide with a 3'-phosphonoacetate group, a 2'-O-methyl nucleotide with a 3'-thiophosphonocarboxylate group, a 2'-O-methyl nucleotide with a 3'-thiophosphonoacetate group, a 2'-deoxy nucleotide with a 3'-phosphonoacetate group, a 2'-deoxy nucleotide with a 3'-thiophosphonoacetate group, and a Z base.

B4. The synthetic guide RNA of embodiment 1, 2 or 3, comprising one or more modifications selected from the group consisting of a 2'-fluororibosyl, a 2-thiouracil base, a 4-thiouracil base, a 2-aminoadenine base, an hypoxanthine base, a 5-methylcytosine base, a 5-methyluracil base, a methylphosphonate internucleotide linkage, a 5-aminoallyluracil base, a squarate linkage, a triazolo linkage, a dye conjugated to a nucleotide, and combinations thereof.

B5. The synthetic guide RNA of any of the preceding embodiments, comprising a modification selected from the group consisting of a 2'-MOE, 2'-amino, 2'-F-arabino, 2'-LNA, 2'-ULNA, 3'-methylphosphonate, 3'-boranophosphonate, 3'-phosphorodithioate, 2'-OMe-3'-P($S)_2$, 2'-OMe-3'-P(CH_3), 2'-OMe-3'-P(BH_3), 4'-thioribosyl, L-sugar, 2-thiocytosine, 6-thioguanine, 2-aminopurine, pseudouracil, 7-deazaguanine, 7-deaza-8-azaguanine, 7-deazaadenine, 7-deaza-8-azaadenine, 5-hydroxymethylcytosine, 5-hydroxymethyluracil, 5,6-dehydrouracil, 5-propynylcytosine, 5-propynyluracil, 5-ethynylcytosine, 5-ethynyluracil, 5-allyluracil, 5-allylcytosine, 5-allylaminocytosine, P nucleobase, isocytosine (isoC), isoguanine (isoG),UNA, x(A,G,C,T), y(A,G,C,T), abasic nucleotide, PEG, hydrocarbon linker, halo-substituted hydrocarbon linker, heteroatom (O,N,S)-substituted hydrocarbon linker, (keto, carboxy, amido, thionyl, carbamoyl, or thionocarbamoyl)-containing hydrocarbon linker, spermine linker, and combinations thereof.

B6. The synthetic guide RNA of any one of the preceding embodiments, comprising a stability-enhancing modification.

B7. The synthetic guide RNA of any one of the preceding embodiments, comprising at least two modifications; wherein a first modification is a stability-enhancing modification and a second modification is a specificity-altering modification.

B8. The synthetic guide RNA of embodiment 6 or 7, wherein the stability-enhancing modification is located in the guide sequence.

B9. The synthetic guide RNA of embodiment 6 or 7, wherein the stability-enhancing modification is located upstream of the guide sequence.

B10. The synthetic guide RNA of embodiment 6 or 7, wherein the stability-enhancing modification is located within the first five and/or the last five nucleotides of the crRNA segment.

B11. The synthetic guide RNA of embodiment 6 or 7, wherein the stability-enhancing modification is located in the tracrRNA segment.

B12. The synthetic guide RNA of embodiment 6 or 7, wherein the stability-enhancing modification is located within the first five and/or the last five nucleotides of the tracrRNA segment.

B13. The synthetic guide RNA of any one of embodiments 6-12, wherein the stability-enhancing modification comprises a 2'-O-methyl moiety, a 2'-fluoro moiety, or a 2'-deoxy moiety.

B14. The synthetic guide RNA of any one of embodiments 6-13, wherein the stability-enhancing modification comprises a phosphorothioate internucleotide linkage, a phosphonoacetate internucleotide linkage, a thiophosphonoacetate internucleotide linkage, a methylphosphonate internucleotide linkage, a boranophosphate internucleotide linkage, or a phosphorodithioate internucleotide linkage.

B15. The synthetic guide RNA of any one of embodiments 6-14, wherein the stability-enhancing modification comprises a 3'-phosphonoacetate or a 3'-thiophosphonoacetate.

B16. The synthetic guide RNA any one of embodiments 6-15, wherein the stability-enhancing modification comprises a 2'-O-methyl-3'-phosphorothioate nucleotide, a 2'-O-methyl-3'-phosphonoacetate nucleotide, or a 2'-O-methyl-3'-thiophosphonoacetate nucleotide.

B17. The synthetic guide RNA of any one of embodiments 6-16, wherein the stability-enhancing modification comprises a 2'-fluoro-3'-phosphorothioate nucleotide, a 2'-fluoro-3'-phosphonoacetate nucleotide, or a 2'-fluoro-3'-thiophosphonoacetate nucleotide.

B18. The synthetic guide RNA of any one of the preceding embodiments, comprising a specificity-altering modification.

B19. The synthetic guide RNA of embodiment 18, wherein the specificity-altering modification is located in the guide sequence.

B20. The synthetic guide RNA of any one of embodiment 18 or 19, wherein the specificity-altering modification comprises a 2-thiouracil, a 4-thiouracil or a 2-aminoadenine.

B21. The synthetic guide RNA of any one of embodiments 18-20, wherein the specificity-altering modification comprises a phosphorothioate internucleotide linkage, a phosphonoacetate internucleotide linkage, a thiophosphono-

acetate internucleotide linkage, a methylphosphonate internucleotide linkage, a boranophosphate internucleotide linkage, or a phosphorodithioate internucleotide linkage.

B22. The synthetic guide RNA of any one of embodiments 18-21, wherein the specificity-altering modification comprises a 3'-phosphonoacetate or a 3'-thiophosphonoacetate.

B23. The synthetic guide RNA of any one of the preceding embodiments, comprising a fluorescent dye or a label.

B24. The synthetic guide RNA of any one of the preceding embodiments, comprising one or more isotopic labels.

B25. The synthetic guide RNA of any one of the preceding embodiments, wherein the guide RNA is conjugated to an oligonucleotide, an aptamer, an amino acid, a peptide, a protein, a steroid, a lipid, a folic acid, a vitamin, a sugar, or an oligosaccharide.

B26. The synthetic guide RNA of any one of the preceding embodiments, wherein the synthetic guide RNA is a single guide RNA, wherein the crRNA segment and the tracrRNA segment are linked through a loop L.

B27. The synthetic guide RNA of embodiment 26, wherein the loop L comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides.

B28. The synthetic guide RNA of embodiment 26 or 27, wherein the loop L comprises a nucleotide sequence of GNRA, wherein N represents A, C, G, or U and R represents A or G.

B29. The synthetic guide RNA of embodiment 26, 27 or 28, wherein the loop L comprises a nucleotide sequence of GAAA.

B30. The synthetic guide RNA of any one of embodiments 26-29, wherein the loop L comprises one or more modified nucleotides.

B31. The synthetic guide RNA of embodiment 30, wherein the loop L comprises a fluorescent dye.

B32. The synthetic guide RNA of embodiment 31, wherein the dye is conjugated to a 2-(4-butylamido-dye) propane-1,3-diol bis(phosphodiester) linker.

B33. The synthetic guide RNA of any one of the preceding embodiments, wherein the crRNA segment is at the 5' end of the guide RNA.

B34. The synthetic guide RNA of any one of the preceding embodiments, wherein the tracrRNA segment is at the 3' end of the guide RNA.

B35. The synthetic guide RNA of any of the preceding embodiments, wherein the crRNA segment comprises from 25 to 70 nucleotides.

B36. The synthetic guide RNA of any of the preceding embodiments, wherein the guide sequence comprises from 15 to 30 nucleotides.

B37. The synthetic guide RNA of any of the preceding embodiments, wherein the stem sequence comprises from 10 to 50 nucleotides.

B38. The synthetic guide RNA of any of the preceding embodiments, comprising one or more triazolo linkage(s).

B39. The synthetic guide RNA of any of the preceding embodiments, comprising one or more squarate linkage(s).

B40. The synthetic guide RNA of any of the preceding embodiments, wherein the guide RNA comprises a nucleotide composition of:

$$M_mN_n$$

wherein each N independently represents an unmodified nucleotide and each M is selected from a 2'-O-methyl ribonucleotide, a 2'-O-methyl-3'-P(S) ribonucleotide, a 2'-O-methyl-3'-PACE ribonucleotide, a 2'-O-methyl-3'-thioPACE ribonucleotide, and a 2'-deoxynucleotide;

wherein each M is at any position in the sequence of the guide RNA; and

wherein m is an integer between 1 and 220, and n is an integer between 0 and 219, and $50<m+n\leq 220$.

B41. The synthetic guide RNA of embodiment 38, wherein $m+n\leq 150$, and each of m and n are independently selected from an integer between 0 and 150, provided that m is not 0.

B42. The synthetic guide RNA of any of the preceding embodiments, wherein the guide RNA comprises a nucleotide sequence of:

$$M_mN_nM'_mN'_nM''_{m''}$$

wherein each M, M' and M" independently represent a modified nucleotide and each N and N' independently represent an unmodified ribonucleotide;

wherein any given M is the same or different from any other M, any given N is the same or different from any other N, any given M' is the same or different from any other M', any given N' is the same or different from any other N', any given M" is the same or different from any other M"; and wherein m is an integer between 0 and 40, n is an integer between 20 and 130, m' is an integer between 0 and 10, n' is an integer between 0 and 50, m" is an integer between 0 and 10, provided that m+m'+m" is greater than or equal to 1.

B43. The synthetic guide RNA of any of the preceding embodiments, wherein the crRNA segment comprises a nucleotide sequence of:

$$M_mN_nM'_mN'_{n'}$$

wherein M and M' each represent a modified nucleotide and N and N' each represent an unmodified ribonucleotide; wherein any given M is the same or different from any other M, any given N is the same or different from any other N, any given M' is the same or different from any other M', any given N' is the same or different from any other N'; and

wherein n and n' are each independently selected from an integer between 0 and 50, and wherein m and m' are each independently selected from an integer between 0 and 25, provided that m+m' is greater than or equal to 1.

B44. The synthetic guide RNA of any of the preceding embodiments, wherein the guide sequence comprises a nucleotide sequence of:

$$M_mN_nM'_mN'_{n'}$$

wherein M and M' each represent a modified nucleotide and N and N' each represent an unmodified ribonucleotide;

wherein any given M is the same or different from any other M, any given N is the same or different from any other N, any given M' is the same or different from any other M', any given N' is the same or different from any other N'; and

wherein m, n, m', and n' are each independently selected from an integer between 0 and 40, provided that m+m' is greater than or equal to 1.

B45. The synthetic guide RNA of any of the preceding embodiments, wherein the tracrRNA segment comprises a nucleotide sequence of:

$$N_nM_mN'_nM'_{m'}$$

wherein M and M' each represent a modified nucleotide and N and N' each represent an unmodified ribonucleotide;

wherein any given M is the same or different from any other M, any given N is the same or different from any other N, any given M' is the same or different from any other M', any given N' is the same or different from any other N'; and

wherein n is an integer between 0 and 130 m is an integer between 0 and 40, and n' is an integer between 0 and 130, and m' is an integer between 0 and 40, provided that m+m' is greater than or equal to 1.

B46. The synthetic guide RNA of any one of embodiments 40-43, wherein m, m', m+m', or m+m'+m" is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20.

B47. The synthetic guide RNA of any one of embodiments 40-43, wherein m, m', m+m', or m+m'+m" is 1, 2, 3, 4, 5, or 6.

B48. The synthetic guide RNA of any one of embodiments 40-45, wherein n is 16, 17, 18, or 19.

B49. The synthetic guide RNA of any one of embodiments 40-45, wherein n, n', or n+n' is an integer between 75 and 115.

B50. The synthetic guide RNA of any one of embodiments 40-47, wherein each M is independently selected from the group consisting of a 2'-modified nucleotide, a 3'-modified nucleotide, and combinations thereof.

B51. The synthetic guide RNA of embodiment 48, wherein the 2'-modified nucleotide is selected from the group consisting of a 2'-deoxy nucleotide, a 2'-O-methyl nucleotide, a 2'-fluoro nucleotide, and a 2'-O—C_{1-3}alkyl-O—C_{1-3}alkyl nucleotide.

B52. The synthetic guide RNA of embodiment 48, wherein the 3'-modified nucleotide is selected from the group consisting of a 3'-phosphonoacetate nucleotide and a 3'-thiophosphonoacetate nucleotide.

B53. The synthetic guide RNA of embodiment 48, wherein the combination of the 2'-modified nucleotide and the 3'-modified nucleotide comprises a 2'-O-methyl-3'-phosphorothioate nucleotide, a 2'-O-methyl-3'-phosphonoacetate nucleotide, or a 2'-O-methyl-3'-thiophosphonoacetate nucleotide.

B54. A method for cleaving a target polynucleotide comprising contacting the target polynucleotide with a CRISPR-associated protein and the synthetic guide RNA of any one of the preceding embodiments and cleaving the target polynucleotide.

B55. The method of embodiment 52, further comprising contacting the target polynucleotide with an exogenous CRISPR-associated protein.

B56. The method of embodiment 53, wherein the CRISPR-associated protein is Cas9.

B57. The method of any one of embodiments 52-54, wherein the cleavage results in a functional knockout of a target gene.

B58. The method of any one of embodiments 52-55, further comprising repairing the cleaved target polynucleotide by homology-directed repair with an exogenous or endogenous template polynucleotide.

B59. The method of embodiment 56, wherein the exogenous or endogenous template polynucleotide comprises at least one sequence having substantial sequence identity with a sequence on either side of the cleavage site.

B60. The method of any one of embodiments 52-57, further comprising repairing the cleaved target polynucleotide by non-homologous end joining.

B61. The method of any one of embodiments 56-58, wherein the repairing step produces an insertion, deletion, or substitution of one or more nucleotides of the target polynucleotide.

B62. The method of embodiment 59, wherein the insertion, deletion, or substitution results in one or more amino acid changes in a protein expressed from a gene comprising the target polynucleotide.

B63. The method of any one of embodiments 52-60, wherein the target polynucleotide is contacted with the CRISPR-associated protein and the synthetic guide RNA in vitro.

B64. The method of any one of embodiments 52-61, wherein the target polynucleotide contacted with the CRISPR-associated protein and the synthetic guide RNA is within the genome of a cell in vitro or in vivo.

B65. The method of embodiment 62, wherein the cell is isolated from a multicellular source prior to contacting the target polynucleotide with the CRISPR-associated protein and the synthetic guide RNA.

B66. The method of embodiment 63, wherein the source is a plant, an animal, a multicellular protist, or a fungus.

B67. The method of any one of embodiments 62-64, wherein the cell, or a cell derived therefrom, is returned to the source after contacting the target polynucleotide with the CRISPR-associated protein and the synthetic guide RNA.

B68. A method of modifying a target polynucleotide in a cell comprising introducing into the cell the synthetic guide RNA of any one of embodiments 1-51 and introducing into the cell a CRISPR-associated protein or a nucleic acid that expresses a CRISPR-associated protein in the cell.

B69. The method of embodiment 66, wherein the CRISPR-associated-protein is Cas9.

B70. A method of altering expression of at least one gene product in a cell comprising introducing into the cell the synthetic guide RNA of any one of embodiments 1-51 and further introducing into the cell a CRISPR-associated-protein or a nucleic acid that expresses a CRISPR-associated protein in the cell, wherein the cell contains and expresses a DNA molecule having a target sequence and encoding the gene product.

B71. The method of embodiment 68, wherein the CRISPR-associated-protein is Cas9.

B72. The method of embodiment 69, wherein the CRISPR-associated-protein cleaves the DNA molecule.

B73. A set or library of RNA molecules comprising two or more synthetic guide RNAs of any one of embodiments 1-51.

B74. A kit comprising the synthetic guide RNA of any one of embodiments 1-51 or the set or library of RNA molecules of embodiment 71.

B75. The kit of embodiment 72, further comprising a CRISPR-associated protein or a nucleic acid encoding the CRISPR-associated protein.

B76. The kit of embodiment 73, wherein the CRISPR-associated-protein is Cas9.

B77. The synthetic guide RNA, method or kit of any of the preceding embodiments, wherein the synthetic guide RNA comprises an end modification.

B78. The synthetic guide RNA of any of the preceding embodiments, having a single RNA strand or two separate complementary RNA strands, wherein the guide RNA comprises at least one stability-enhancing modification at both ends of each RNA strand.

C1. A synthetic guide RNA comprising:

(a) a crRNA segment comprising (i) a guide sequence capable of hybridizing to a target sequence in a polynucleotide, (ii) a stem sequence; and

(b) a tracrRNA segment comprising a nucleotide sequence that is partially or completely complementary to the stem sequence, wherein the synthetic guide RNA comprises one or more modifications, and wherein the synthetic guide RNA has gRNA functionality.

C2. The synthetic guide RNA of embodiment C1, wherein one or more of the modifications comprises a stability-enhancing modification.

C3. The synthetic guide RNA of embodiment C2, wherein one or more of the stability-enhancing modifications is located in the guide sequence.

C4. The synthetic guide RNA of embodiment C2, wherein the stability-enhancing modification comprises a 2'-O-methyl moiety, a Z base, a 2'-deoxy nucleotide, a phosphorothioate internucleotide linkage, a phosphonoacetate (PACE) internucleotide linkage, or a thiophosphonoacetate (thioPACE) internucleotide linkage, or combinations thereof.

C5. The synthetic guide RNA of any of the foregoing embodiments, comprising less than 26 consecutive 2'-O-methyl modified nucleotides at a 5' end of the guide RNA.

C6. The synthetic guide RNA of any of the foregoing embodiments, comprising a Z base replacing a cytosine in the synthetic guide RNA.

C7. The synthetic guide RNA of any of the foregoing embodiments, comprising at least one 2-thiouracil at a position corresponding to a uridine that can engage in U-G wobble pairing with a potential off-target sequence.

C8. The synthetic guide RNA of any of the foregoing embodiments, comprising one or more modifications selected from the group consisting of a 2'-O-methyl nucleotide with a 3'-phosphorothioate group, a 2'-O-methyl nucleotide with a 3'-phosphonoacetate group, a 2'-O-methyl nucleotide with a 3'-thiophosphonoacetate group, and a 2'-deoxy nucleotide with a 3'-phosphonoacetate group.

C9. The synthetic guide RNA of any of the foregoing embodiments, comprising at least two modifications.

C10. The synthetic guide RNA any of the foregoing embodiments, comprising up to 50 modifications.

C11. The synthetic guide RNA of any of the foregoing embodiments, comprising a single RNA strand or two separate RNA strands, and one or more modifications at a 5' end of each RNA strand, at a 3' end of each RNA strand, or at both a 5' end and a 3' end of each RNA strand.

C12. The synthetic guide RNA of any of the foregoing embodiments, comprising 7 or fewer consecutive modified nucleotides at a 5' end or at a 3' end or at each of 5' and 3' ends.

C13. The synthetic guide RNA of any of the foregoing embodiments, comprising one or more 5-methyluridine nucleotides at one or more of a 5' end, a 3' end, or a stem-loop.

C14. The synthetic guide RNA of any of the foregoing embodiments, wherein one or more of the modifications alters base-pairing thermostability.

C15. The synthetic guide RNA of embodiment C14, wherein said one or more modifications enhances the base-pairing thermostability.

C16. The synthetic guide RNA of embodiment C15, wherein said one or more modifications is independently selected from a 2-thiouracil (2-thioU), a 4-thiouracil (4-thioU), a 2-aminoadenine, a 2'-O-methyl, a 2'-fluoro, a 5-methyluridine, a 5-methylcytidine, and a locked nucleic acid modification (LNA).

C17. The synthetic guide RNA of embodiment C15, wherein said one or more modifications decreases the base-pairing thermostability.

C18. The synthetic guide RNA of embodiment C17, wherein said one or more modifications is independently selected from a 2-thiouracil, a 2'-deoxy, a phosphorothioate linkage, a phosphorodithioate linkage, a boranophosphonate linkage, a phosphonoacetate linkage, a thiophosphonoacetate linkage, and an unlocked nucleic acid modification (ULNA).

C19. The synthetic guide RNA of any of the foregoing embodiments, comprising one or more 2'-O-methylA-2'-O-methylU base pairs.

C20. The synthetic guide RNA of any of the foregoing embodiments, wherein one or more of the modifications is a specificity-altering modification.

C21. The synthetic guide RNA of embodiment C20, wherein the specificity-altering modification is located in the guide sequence.

C22. The synthetic guide RNA of any of the foregoing embodiments, wherein the specificity-altering modification comprises a 2-thiouracil, a 4-thiouracil, a 2-aminoadenine, a 2'-O-methyl, a 2'-fluoro, a LNA, a phosphorothioate linkage, a phosphorodithioate linkage, a boranophosphonate linkage, a phosphonoacetate linkage, a thiophosphonoacetate linkage, an ULNA, a 2'-deoxy, a 5-methyluridine, a 5-methylcytidine, or combinations thereof.

C23. The synthetic guide RNA of any of the foregoing embodiments, comprising a fluorescent dye or a label.

C24. The synthetic guide RNA of embodiment C23, wherein the fluorescent dye or a label is bound to a stem-loop of the synthetic guide RNA.

C25. A method for genomic editing to modify a DNA sequence, or regulating the expression of a gene of interest, or cleaving a target polynucleotide comprising: contacting the DNA sequence, the gene of interest, or the target polynucleotide with a CRISPR-associated protein and the synthetic guide RNA of any of the foregoing embodiments, and editing, regulating or cleaving the DNA sequence, the gene of interest or the target polynucleotide.

C26. The method of embodiment C25, wherein the method is performed in vitro, and the synthetic guide RNA comprises 15 or more 2'-O-methyl modifications throughout the guide sequence.

C27. A set or library of RNA molecules comprising two or more synthetic guide RNAs of any of the foregoing embodiments.

C28. A kit comprising the synthetic guide RNA of any of the foregoing embodiments.

C29. An array of RNA molecules comprising two or more synthetic guide RNAs of any of the foregoing embodiments.

The foregoing description of exemplary or preferred embodiments should be taken as illustrating, rather than as limiting, the present invention as defined by the claims. As will be readily appreciated, numerous variations and combinations of the features set forth above can be utilized without departing from the present invention as set forth in the claims. Such variations are not regarded as a departure from the scope of the invention, and all such variations are intended to be included within the scope of the following claims. All references cited herein are incorporated by reference in their entireties.

SEQUENCE LISTING

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<212> TYPE: PRT
<213> ORGANISM: Streptococcus pyogenes

<400> SEQUENCE: 1

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Lys Val Leu Gly Asn Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile
        35                  40                  45

Gly Ala Leu Leu Phe Asp Ser Gly Glu Thr Ala Glu Ala Thr Arg Leu
    50                  55                  60

Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys
65                  70                  75                  80

Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser
                85                  90                  95

Phe Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys
            100                 105                 110

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
        115                 120                 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
    130                 135                 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
145                 150                 155                 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
                165                 170                 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
            180                 185                 190

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
        195                 200                 205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
    210                 215                 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
225                 230                 235                 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
                245                 250                 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
            260                 265                 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
        275                 280                 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
    290                 295                 300

Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
305                 310                 315                 320

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
                325                 330                 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
            340                 345                 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
        355                 360                 365
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Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
    370                 375                 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
385                 390                 395                 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
                405                 410                 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
            420                 425                 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
        435                 440                 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
    450                 455                 460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
465                 470                 475                 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
                485                 490                 495

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
            500                 505                 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys
        515                 520                 525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
    530                 535                 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
545                 550                 555                 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
                565                 570                 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
            580                 585                 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
        595                 600                 605

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
    610                 615                 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
625                 630                 635                 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
                645                 650                 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
            660                 665                 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
        675                 680                 685

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
    690                 695                 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
705                 710                 715                 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
                725                 730                 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
            740                 745                 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
        755                 760                 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
    770                 775                 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
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785                 790                 795                 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
                805                 810                 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
            820                 825                 830

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
        835                 840                 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
    850                 855                 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
865                 870                 875                 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
                885                 890                 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
            900                 905                 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
        915                 920                 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
    930                 935                 940

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
945                 950                 955                 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
                965                 970                 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
            980                 985                 990

Val Gly Thr Ala Leu Ile Lys Lys  Tyr Pro Lys Leu Glu  Ser Glu Phe
        995                 1000                1005

Val Tyr  Gly Asp Tyr Lys Val  Tyr Asp Val Arg Lys  Met Ile Ala
    1010                1015                1020

Lys Ser  Glu Gln Glu Ile Gly  Lys Ala Thr Ala Lys  Tyr Phe Phe
    1025                1030                1035

Tyr Ser  Asn Ile Met Asn Phe  Phe Lys Thr Glu Ile  Thr Leu Ala
    1040                1045                1050

Asn Gly  Glu Ile Arg Lys Arg  Pro Leu Ile Glu Thr  Asn Gly Glu
    1055                1060                1065

Thr Gly  Glu Ile Val Trp Asp  Lys Gly Arg Asp Phe  Ala Thr Val
    1070                1075                1080

Arg Lys  Val Leu Ser Met Pro  Gln Val Asn Ile Val  Lys Lys Thr
    1085                1090                1095

Glu Val  Gln Thr Gly Gly Phe  Ser Lys Glu Ser Ile  Leu Pro Lys
    1100                1105                1110

Arg Asn  Ser Asp Lys Leu Ile  Ala Arg Lys Lys Asp  Trp Asp Pro
    1115                1120                1125

Lys Lys  Tyr Gly Gly Phe Asp  Ser Pro Thr Val Ala  Tyr Ser Val
    1130                1135                1140

Leu Val  Val Ala Lys Val Glu  Lys Gly Lys Ser Lys  Lys Leu Lys
    1145                1150                1155

Ser Val  Lys Glu Leu Leu Gly  Ile Thr Ile Met Glu  Arg Ser Ser
    1160                1165                1170

Phe Glu  Lys Asn Pro Ile Asp  Phe Leu Glu Ala Lys  Gly Tyr Lys
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Glu Val  Lys Lys Asp Leu Ile  Ile Lys Leu Pro Lys  Tyr Ser Leu
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Phe Glu  Leu Glu Asn Gly Arg  Lys Arg Met Leu Ala  Ser Ala Gly
    1205                 1210                 1215

Glu Leu  Gln Lys Gly Asn Glu  Leu Ala Leu Pro Ser  Lys Tyr Val
    1220                 1225                 1230

Asn Phe  Leu Tyr Leu Ala Ser  His Tyr Glu Lys Leu  Lys Gly Ser
    1235                 1240                 1245

Pro Glu  Asp Asn Glu Gln Lys  Gln Leu Phe Val Glu  Gln His Lys
    1250                 1255                 1260

His Tyr  Leu Asp Glu Ile Ile  Glu Gln Ile Ser Glu  Phe Ser Lys
    1265                 1270                 1275

Arg Val  Ile Leu Ala Asp Ala  Asn Leu Asp Lys Val  Leu Ser Ala
    1280                 1285                 1290

Tyr Asn  Lys His Arg Asp Lys  Pro Ile Arg Glu Gln  Ala Glu Asn
    1295                 1300                 1305

Ile Ile  His Leu Phe Thr Leu  Thr Asn Leu Gly Ala  Pro Ala Ala
    1310                 1315                 1320

Phe Lys  Tyr Phe Asp Thr Thr  Ile Asp Arg Lys Arg  Tyr Thr Ser
    1325                 1330                 1335

Thr Lys  Glu Val Leu Asp Ala  Thr Leu Ile His Gln  Ser Ile Thr
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Gly Leu  Tyr Glu Thr Arg Ile  Asp Leu Ser Gln Leu  Gly Gly Asp
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<212> TYPE: PRT
<213> ORGANISM: Simian virus 40

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<213> ORGANISM: Simian virus 40

<400> SEQUENCE: 3

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<210> SEQ ID NO 4
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

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<212> TYPE: PRT
<213> ORGANISM: Human immunodeficiency virus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: tat protein

<400> SEQUENCE: 5
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<212> TYPE: PRT
<213> ORGANISM: Hepatitis B virus
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: middle S protein, partial

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1               5                   10                  15

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            20                  25


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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 9

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1               5                   10                  15

Lys Lys Arg Lys Val
            20


<210> SEQ ID NO 10
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<220> FEATURE:
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gttctgtcga ccatgtgccg cggattgaat tcctcaaggg tggtgataga tgctacggtg 180

gtgatgcgca tgcgctcagt cctcatctcc ctcaagcagg ccccgctggt gggtcggagt 240

ccctagtgaa gccaccaata tagtggtcgt gtcaagcaac tgtccacgct ccaccctcga 300

ggtcgtaaca taaacgtact aaggcacgag taaacaagat cgatagcaag aacatggtat 360

agactgacgg agagctcgcc attagtctga 390

<210> SEQ ID NO 11
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<220> FEATURE:
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<400> SEQUENCE: 11

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gttctgtcga ccatgtgccg cggattgaat tcctcaaggg tggtgataga tgctacggtg 180

gtgatgcgta tgcactcagt cctcaactcc ctcaagcagg cgacccctgg gggtcggagt 240

ccctagtgaa gccaccaata tagtggtcgt gtcaagcaac tgtccacgct ccaccctcga 300

ggtcgtaaca taaacgtact aaggcacgag taaacaagat cgatagcaag aacatggtat 360

agactgacgg agagctcgcc attagtctga 390

<210> SEQ ID NO 12
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 12

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gcaagttcga tgagtatgcc agtcactttc aatttggttg aatgttcccg tgacatgcga 120

gttctgtcga ccatgtgccg cggattgaat tcctcaaggg tggtgataga tgctacggtg 180

gtgatgcaat aaatttcagc cctcatttcc ctcaagcagg ggttacttta gggtcggagt 240

ccctagtgaa gccaccaata tagtggtcgt gtcaagcaac tgtccacgct ccaccctcga 300

ggtcgtaaca taaacgtact aaggcacgag taaacaagat cgatagcaag aacatggtat 360

agactgacgg agagctcgcc attagtctga 390

<210> SEQ ID NO 13
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 13

agaatttaac tgtggtcaca tttgctttat cgactggctt catctcacag ctcatcttac 60

gcaagttcga tgagtatgcc agtcactttc aatttggttg aatgttcccg tgacatgcga 120

gttctgtcga ccatgtgccg cggattgaat tcctcaaggg tggtgataga tgctacggtg 180

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gtgatgctct ccagcccact cctcatcccc ctcaagccgg tcccaggctg gggtcggagt 240

ccctagtgaa gccaccaata tagtggtcgt gtcaagcaac tgtccacgct ccaccctcga 300

ggtcgtaaca taaacgtact aaggcacgag taaacaagat cgatagcaag aacatggtat 360

agactgacgg agagctcgcc attagtctga 390

<210> SEQ ID NO 14
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 14

gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataagggcga 60

cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg 120

gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg 180

ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa 240

attcgcgtta aatttttgtt aaatcagctc attttttaac caataggccg aaatcggcaa 300

aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa 360

caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca 420

gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg 480

taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc 540

ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta gggcgctggc 600

aagtgtagcg gtcacgctgc gcgtaaccac cacacccgcc gcgcttaatg cgccgctaca 660

gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggtgcgggc 720

ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 780

aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgagc gcgcgtaata 840

cgactcacta tagggcgaat tgggtacgat cgatgcggcc tcgcaggcca aagatgtctc 900

ccgcatgcgc tcagtcctca tctccctcaa gcaggccctg ctggtgcact gaagagccac 960

cctgtgcgcg tgatatgcag ctccagcttt tgttcccttt agtgagggtt aattgcgcgc 1020

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cacaacatac gagccggaag cataaagtgt aaagcctggg gtgcctaatg agtgagctaa 1140

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tgagcaaaag gccagcaaaa ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc 1440

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aacccgacag gactataaag ataccaggcg tttccccctg gaagctccct cgtgcgctct 1560

cctgttccga ccctgccgct taccggatac ctgtccgcct ttctcccttc gggaagcgtg 1620

gcgctttctc atagctcacg ctgtaggtat ctcagttcgg tgtaggtcgt tcgctccaag 1680

ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat 1740

cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac 1800

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aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac 1860

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ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt 1980

tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 2040

ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg 2100

agattatcaa aaaggatctt cacctagatc cttttaaatt aaaaatgaag ttttaaatca 2160

atctaaagta tatatgagta aacttggtct gacagttacc aatgcttaat cagtgaggca 2220

cctatctcag cgatctgtct atttcgttca tccatagttg cctgactccc cgtcgtgtag 2280

ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac 2340

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gttgtcagaa gtaagttggc cgcagtgtta tcactcatgg ttatggcagc actgcataat 2700

tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag 2760

tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat 2820

aataccgcgc cacatagc 2838

<210> SEQ ID NO 15
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 15

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cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg 120

gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg 180

ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa 240

attcgcgtta aatttttgtt aaatcagctc atttttttaac caataggccg aaatcggcaa 300

aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa 360

caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca 420

gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg 480

taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc 540

ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta gggcgctggc 600

aagtgtagcg gtcacgctgc gcgtaaccac cacacccgcc gcgcttaatg cgccgctaca 660

gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggtgcgggc 720

ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 780

aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgagc gcgcgtaata 840

cgactcacta tagggcgaat tgggtacgat cgatgcggcc tcgcagggca aagaggtctc 900

ctgtatgcac tcagtcctca actccctcaa gcaggcgacc cttggtgcac tgacaaaccg 960

ctcctgcgcg tgatatgcag ctccagcttt tgttcccttt agtgagggtt aattgcgcgc 1020

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ttggcgtaat catggtcata gctgtttcct gtgtgaaatt gttatccgct cacaattcca 1080

cacaacatac gagccggaag cataaagtgt aaagcctggg gtgcctaatg agtgagctaa 1140

ctcacattaa ttgcgttgcg ctcactgccc gctttccagt cgggaaacct gtcgtgccag 1200

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cactcaaagg cggtaatacg gttatccaca gaatcagggg ataacgcagg aaagaacatg 1380

tgagcaaaag gccagcaaaa ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc 1440

cataggctcc gccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga 1500

aacccgacag gactataaag ataccaggcg tttccccctg gaagctccct cgtgcgctct 1560

cctgttccga ccctgccgct taccggatac ctgtccgcct ttctcccttc gggaagcgtg 1620

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ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat 1740

cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac 1800

aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac 1860

tacggctaca ctagaaggac agtatttggt atctgcgctc tgctgaagcc agttaccttc 1920

ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt 1980

tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 2040

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agattatcaa aaaggatctt cacctagatc cttttaaatt aaaaatgaag ttttaaatca 2160

atctaaagta tatatgagta aacttggtct gacagttacc aatgcttaat cagtgaggca 2220

cctatctcag cgatctgtct atttcgttca tccatagttg cctgactccc cgtcgtgtag 2280

ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac 2340

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gttgtcagaa gtaagttggc cgcagtgtta tcactcatgg ttatggcagc actgcataat 2700

tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag 2760

tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat 2820

aataccgcgc cacatagc 2838

<210> SEQ ID NO 16
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 16

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cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg 120

gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg 180

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ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa    240
attcgcgtta aatttttgtt aaatcagctc atttttttaac caataggccg aaatcggcaa    300
aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa    360
caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca    420
gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg    480
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cacaacatac gagccggaag cataaagtgt aaagcctggg gtgcctaatg agtgagctaa   1140
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ctgcattaat gaatcggcca acgcgcgggg agaggcggtt tgcgtattgg gcgctcttcc   1260
gcttcctcgc tcactgactc gctgcgctcg gtcgttcggc tgcggcgagc ggtatcagct   1320
cactcaaagg cggtaatacg gttatccaca gaatcagggg ataacgcagg aaagaacatg   1380
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cataggctcc gccccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga   1500
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gcgctttctc atagctcacg ctgtaggtat ctcagttcgg tgtaggtcgt tcgctccaag   1680
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aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac   1860
tacggctaca ctagaaggac agtatttggt atctgcgctc tgctgaagcc agttaccttc   1920
ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt   1980
tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc   2040
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ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac   2340
ccacgctcac cggctccaga tttatcagca ataaaccagc cagccggaag ggccgagcgc   2400
agaagtggtc ctgcaacttt atccgcctcc atccagtcta ttaattgttg ccgggaagct   2460
agagtaagta gttcgccagt taatagtttg cgcaacgttg ttgccattgc tacaggcatc   2520
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tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag 2760

tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat 2820

aataccgcgc cacatagc 2838

<210> SEQ ID NO 17
<211> LENGTH: 2995
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 17

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tcaccagtca cagaaaagca tcttacggat ggcatgacag taagagaatt atgcagtgct 120

gccataacca tgagtgataa cactgcggcc aacttacttc tgacaacgat cggaggaccg 180

aaggagctaa ccgcttttt gcacaacatg ggggatcatg taactcgcct tgatcgttgg 240

gaaccggagc tgaatgaagc cataccaaac gacgagcgtg acaccacgat gcctgtagca 300

atggcaacaa cgttgcgcaa actattaact ggcgaactac ttactctagc ttcccggcaa 360

caattaatag actggatgga ggcggataaa gttgcaggac cacttctgcg ctcggccctt 420

ccggctggct ggtttattgc tgataaatct ggagccggtg agcgtgggtc tcgcggtatc 480

attgcagcac tggggccaga tggtaagccc tcccgtatcg tagttatcta cacgacgggg 540

agtcaggcaa ctatggatga acgaaataga cagatcgctg agataggtgc ctcactgatt 600

aagcattggt aactgtcaga ccaagtttac tcatatatac tttagattga tttaaaactt 660

catttttaat ttaaaaggat ctaggtgaag atcctttttg ataatctcat gaccaaaatc 720

ccttaacgtg agttttcgtt ccactgagcg tcagaccccg tagaaaagat caaaggatct 780

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ttcagcagag cgcagatacc aaatactgtt cttctagtgt agccgtagtt aggccaccac 960

ttcaagaact ctgtagcacc gccacatacc tcgctctgct aatcctgtta ccagtggctg 1020

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aaggcgcagc ggtcgggctg aacgggggggt tcgtgcacac agcccagctt ggagcgaacg 1140

acctacaccg aactgagata cctacagcgt gagctatgag aaagcgccac gcttcccgaa 1200

gggagaaagg cggacaggta tccggtaagc ggcagggtcg gaacaggaga gcgcacgagg 1260

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cgccgcagcc gaacgaccga gcgcagcgag tcagtgagcg aggaagcgga agagcgccca 1560

atacgcaaac cgcctctccc cgcgcgttgg ccgattcatt aatgcagctg gcacgacagg 1620

tttcccgact ggaaagcggg cagtgagcgc aacgcaatta atgtgagtta gctcactcat 1680

taggcacccc aggctttaca ctttatgctt ccggctcgta tgttgtgtgg aattgtgagc 1740

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ggataacaat ttcacacagg aaacagctat gaccatgatt acgccaagcg cgcaattaac 1800

cctcactaaa gggaacaaaa gctgggtacc gggcccccc tcgacaccag ttgcattcga 1860

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ctggcgttac ccaacttaat cgccttgcag cacatccccc tttcgccagc tggcgtaata 2100

gcgaagaggc ccgcaccgat cgcccttccc aacagttgcg cagcctgaat ggcgaatgga 2160

aattgtaagc gttaatattt tgttaaaatt cgcgttaaat ttttgttaaa tcagctcatt 2220

ttttaaccaa taggccgaaa tcggcaaaat cccttataaa tcaaaagaat agaccgagat 2280

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atcaagtttt ttggggtcga ggtgccgtaa agcactaaat cggaacccta aagggagccc 2460

ccgatttaga gcttgacggg gaaagccggc gaacgtggcg agaaaggaag ggaagaaagc 2520

gaaaggagcg ggcgctaggg cgctggcaag tgtagcggtc acgctgcgcg taaccaccac 2580

acccgccgcg cttaatgcgc cgctacaggg cgcgtcaggt ggcacttttc ggggaaatgt 2640

gcgcggaacc cctatttgtt tatttttcta aatacattca aatatgtatc cgctcatgag 2700

acaataaccc tgataaatgc ttcaataata ttgaaaaagg aagagtatga gtattcaaca 2760

tttccgtgtc gcccttattc cctttttttgc ggcattttgc cttcctgttt ttgctcaccc 2820

agaaacgctg gtgaaagtaa aagatgctga agatcagttg ggtgcacgag tgggttacat 2880

cgaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag aacgttttcc 2940

aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgta ttgac 2995

<210> SEQ ID NO 18
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 18

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aataccgcgc cacatagc 2838

<210> SEQ ID NO 19
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 19

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gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg    180
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aataccgcgc cacatagc 2838

<210> SEQ ID NO 20
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 20

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gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg 180

ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa 240

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aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa 360

caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca 420

gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg 480

taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc 540

ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta gggcgctggc 600

aagtgtagcg gtcacgctgc gcgtaaccac cacacccgcc gcgcttaatg cgccgctaca 660

gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggtgcgggc 720

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aataccgcgc cacatagc 2838

<210> SEQ ID NO 21
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 21

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ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa 240

attcgcgtta aatttttgtt aaatcagctc atttttttaac caataggccg aaatcggcaa 300

aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa 360

caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca 420

gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg 480

taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc 540

ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta gggcgctggc 600

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aataccgcgc cacatagc 2838

<210> SEQ ID NO 22
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

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<400> SEQUENCE: 22

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gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg 180

ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa 240

attcgcgtta aatttttgtt aaatcagctc attttttaac caataggccg aaatcggcaa 300

aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa 360

caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca 420

gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg 480

taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc 540

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ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat 1740

cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac 1800

aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac 1860

tacggctaca ctagaaggac agtatttggt atctgcgctc tgctgaagcc agttaccttc 1920

ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt 1980

tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 2040

ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg 2100

agattatcaa aaaggatctt cacctagatc cttttaaatt aaaaatgaag ttttaaatca 2160

atctaaagta tatatgagta aacttggtct gacagttacc aatgcttaat cagtgaggca 2220

cctatctcag cgatctgtct atttcgttca tccatagttg cctgactccc cgtcgtgtag 2280

ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac 2340

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ccacgctcac cggctccaga tttatcagca ataaaccagc cagccggaag ggccgagcgc 2400

agaagtggtc ctgcaacttt atccgcctcc atccagtcta ttaattgttg ccgggaagct 2460

agagtaagta gttcgccagt taatagtttg cgcaacgttg ttgccattgc tacaggcatc 2520

gtggtgtcac gctcgtcgtt tggtatggct tcattcagct ccggttccca acgatcaagg 2580

cgagttacat gatcccccat gttgtgcaaa aaagcggtta gctccttcgg tcctccgatc 2640

gttgtcagaa gtaagttggc cgcagtgtta tcactcatgg ttatggcagc actgcataat 2700

tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag 2760

tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat 2820

aataccgcgc cacatagc 2838

<210> SEQ ID NO 23
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 23

gcgtttctgg gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataagggcga 60

cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg 120

gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg 180

ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa 240

attcgcgtta aatttttgtt aaatcagctc attttttaac caataggccg aaatcggcaa 300

aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa 360

caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca 420

gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg 480

taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc 540

ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta gggcgctggc 600

aagtgtagcg gtcacgctgc gcgtaaccac cacacccgcc gcgcttaatg cgccgctaca 660

gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggtgcgggc 720

ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 780

aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgagc gcgcgtaata 840

cgactcacta tagggcgaat tgggtacgat cgatgcggcc tcggaacatt ggtaattaaa 900

cttaacgcct cagatttaga cgaaggattg aatggggaca ttgtttattc attctcgaat 960

gatacgcgcg tgatatgcag ctccagcttt tgttcccttt agtgagggtt aattgcgcgc 1020

ttggcgtaat catggtcata gctgtttcct gtgtgaaatt gttatccgct cacaattcca 1080

cacaacatac gagccggaag cataaagtgt aaagcctggg gtgcctaatg agtgagctaa 1140

ctcacattaa ttgcgttgcg ctcactgccc gctttccagt cgggaaacct gtcgtgccag 1200

ctgcattaat gaatcggcca acgcgcgggg agaggcggtt tgcgtattgg gcgctcttcc 1260

gcttcctcgc tcactgactc gctgcgctcg gtcgttcggc tgcggcgagc ggtatcagct 1320

cactcaaagg cggtaatacg gttatccaca gaatcagggg ataacgcagg aaagaacatg 1380

tgagcaaaag gccagcaaaa ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc 1440

cataggctcc gccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga 1500

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aacccgacag gactataaag ataccaggcg tttccccctg gaagctccct cgtgcgctct 1560

cctgttccga ccctgccgct taccggatac ctgtccgcct ttctcccttc gggaagcgtg 1620

gcgctttctc atagctcacg ctgtaggtat ctcagttcgg tgtaggtcgt tcgctccaag 1680

ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat 1740

cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac 1800

aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac 1860

tacggctaca ctagaaggac agtatttggt atctgcgctc tgctgaagcc agttaccttc 1920

ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt 1980

tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 2040

ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg 2100

agattatcaa aaaggatctt cacctagatc cttttaaatt aaaaatgaag ttttaaatca 2160

atctaaagta tatatgagta aacttggtct gacagttacc aatgcttaat cagtgaggca 2220

cctatctcag cgatctgtct atttcgttca tccatagttg cctgactccc cgtcgtgtag 2280

ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac 2340

ccacgctcac cggctccaga tttatcagca ataaaccagc cagccggaag ggccgagcgc 2400

agaagtggtc ctgcaacttt atccgcctcc atccagtcta ttaattgttg ccgggaagct 2460

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cgagttacat gatcccccat gttgtgcaaa aaagcggtta gctccttcgg tcctccgatc 2640

gttgtcagaa gtaagttggc cgcagtgtta tcactcatgg ttatggcagc actgcataat 2700

tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag 2760

tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat 2820

aataccgcgc cacatagc 2838

<210> SEQ ID NO 24
<211> LENGTH: 2838
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 24

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cacggaaatg ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg 120

gttattgtct catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg 180

ttccgcgcac atttccccga aaagtgccac ctaaattgta agcgttaata ttttgttaaa 240

attcgcgtta aatttttgtt aaatcagctc atttttttaac caataggccg aaatcggcaa 300

aatcccttat aaatcaaaag aatagaccga gatagggttg agtgttgttc cagtttggaa 360

caagagtcca ctattaaaga acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca 420

gggcgatggc ccactacgtg aaccatcacc ctaatcaagt tttttggggt cgaggtgccg 480

taaagcacta aatcggaacc ctaaagggag cccccgattt agagcttgac ggggaaagcc 540

ggcgaacgtg gcgagaaagg aagggaagaa agcgaaagga gcgggcgcta gggcgctggc 600

aagtgtagcg gtcacgctgc gcgtaaccac cacacccgcc gcgcttaatg cgccgctaca 660

gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cggtgcgggc 720

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ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt    780

aacgccaggg ttttcccagt cacgacgttg taaaacgacg gccagtgagc gcgcgtaata    840

cgactcacta tagggcgaat tgggtacgat cgatgcggcc tcggaacgct ggtgattcat    900

cccaatgcct cagatttaga cgaaggcttg aatggggata ttatttactc cttctccagt    960

gatgtgcgcg tgatatgcag ctccagcttt tgttcccttt agtgagggtt aattgcgcgc   1020

ttggcgtaat catggtcata gctgtttcct gtgtgaaatt gttatccgct cacaattcca   1080

cacaacatac gagccggaag cataaagtgt aaagcctggg gtgcctaatg agtgagctaa   1140

ctcacattaa ttgcgttgcg ctcactgccc gctttccagt cgggaaacct gtcgtgccag   1200

ctgcattaat gaatcggcca acgcgcgggg agaggcggtt tgcgtattgg gcgctcttcc   1260

gcttcctcgc tcactgactc gctgcgctcg gtcgttcggc tgcggcgagc ggtatcagct   1320

cactcaaagg cggtaatacg gttatccaca gaatcagggg ataacgcagg aaagaacatg   1380

tgagcaaaag gccagcaaaa ggccaggaac cgtaaaaagg ccgcgttgct ggcgtttttc   1440

cataggctcc gccccccctga cgagcatcac aaaaatcgac gctcaagtca gaggtggcga   1500

aacccgacag gactataaag ataccaggcg tttccccctg gaagctccct cgtgcgctct   1560

cctgttccga ccctgccgct taccggatac ctgtccgcct ttctcccttc gggaagcgtg   1620

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ctgggctgtg tgcacgaacc ccccgttcag cccgaccgct gcgccttatc cggtaactat   1740

cgtcttgagt ccaacccggt aagacacgac ttatcgccac tggcagcagc cactggtaac   1800

aggattagca gagcgaggta tgtaggcggt gctacagagt tcttgaagtg gtggcctaac   1860

tacggctaca ctagaaggac agtatttggt atctgcgctc tgctgaagcc agttaccttc   1920

ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt   1980

tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc   2040

ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg   2100

agattatcaa aaaggatctt cacctagatc cttttaaatt aaaaatgaag ttttaaatca   2160

atctaaagta tatatgagta aacttggtct gacagttacc aatgcttaat cagtgaggca   2220

cctatctcag cgatctgtct atttcgttca tccatagttg cctgactccc cgtcgtgtag   2280

ataactacga tacgggaggg cttaccatct ggccccagtg ctgcaatgat accgcgagac   2340

ccacgctcac cggctccaga tttatcagca ataaaccagc cagccggaag ggccgagcgc   2400

agaagtggtc ctgcaacttt atccgcctcc atccagtcta ttaattgttg ccgggaagct   2460

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gtggtgtcac gctcgtcgtt tggtatggct tcattcagct ccggttccca acgatcaagg   2580

cgagttacat gatcccccat gttgtgcaaa aaagcggtta gctccttcgg tcctccgatc   2640

gttgtcagaa gtaagttggc cgcagtgtta tcactcatgg ttatggcagc actgcataat   2700

tctcttactg tcatgccatc cgtaagatgc ttttctgtga ctggtgagta ctcaaccaag   2760

tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat   2820

aataccgcgc cacatagc                                                2838
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<210> SEQ ID NO 25
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 25

aguccucauc ucccucaagc guuuaagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 26
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 26

ggaaccauuc aaaacagcau agcaaguuua aauaaggcua guccguuauc aacuuguaaa 60

aguggcaccg agucggugcu uuuuuu 86

<210> SEQ ID NO 27
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 27

ugguaaugau ggcuucaaca guuuuagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 28
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 28

ggaaccauuc aaaacagcau agcaaguuua aauaaggcua guccguuauc aacuuguaaa 60

aguggcaccg agucggugcu uuuuuu 86

<210> SEQ ID NO 29
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 29

aguccucauc ucccucaagc guuuaagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 30
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (57)..(57)
<223> OTHER INFORMATION: u is 5-(3-Aminoallyl)-uridine-5'-triphosphate, labeled with Cyanine5

<400> SEQUENCE: 30

ggaaccauuc aaaacagcau agcaaguuua aauaaggcua guccguuauc aacuuguaaa 60

aguggcaccg agucggugcu uuuuuu 86

<210> SEQ ID NO 31

<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-methyl
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: 2'-O-methyl
<222> LOCATION: (53)..(55)

<400> SEQUENCE: 31

ugguaaugau ggcuucaaca guuuuagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 32
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl
<222> LOCATION: (83)..(85)

<400> SEQUENCE: 32

ggaaccauuc aaaacagcau agcaaguuua aauaaggcua guccguuauc aacuuguaaa 60

aguggcaccg agucggugcu uuuuuu 86

<210> SEQ ID NO 33
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl
<222> LOCATION: (53)..(55)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (53)..(56)

<400> SEQUENCE: 33

ugguaaugau ggcuucaaca guuuuagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 34
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (83)..(85)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (83)..(86)

<400> SEQUENCE: 34

ggaaccauuc aaaacagcau agcaaguuua aauaaggcua guccguuauc aacuuguaaa 60

aguggcaccg agucggugcu uuuuuu 86

<210> SEQ ID NO 35
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (53)..(55)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (53)..(56)

<400> SEQUENCE: 35

ugguaaugau ggcuucaaca guuuuagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 36
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (83)..(85)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (83)..(86)

<400> SEQUENCE: 36

ggaaccauuc aaaacagcau agcaaguuua aauaaggcua guccguuauc aacuuguaaa 60

aguggcaccg agucggugcu uuuuuu 86

<210> SEQ ID NO 37
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (55)..(55)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (55)..(56)

<400> SEQUENCE: 37

ugguaaugau ggcuucaaca guuuuagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 38
<211> LENGTH: 86
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
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<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (85)..(85)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (85)..(86)

<400> SEQUENCE: 38

ggaaccauuc aaaacagcau agcaaguuua aauaaggcua guccguuauc aacuuguaaa 60

aguggcaccg agucggugcu uuuuuu 86

<210> SEQ ID NO 39
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2-thiouridine nucleotide
<222> LOCATION: (3)..(3)

<400> SEQUENCE: 39

aguccucauc ucccucaagc guuuaagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 40
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2-thiouridine nucleotide
<222> LOCATION: (9)..(9)

<400> SEQUENCE: 40

aguccucauc ucccucaagc guuuaagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 41
<211> LENGTH: 56
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2-thiouridine nucleotide
<222> LOCATION: (11)..(11)

<400> SEQUENCE: 41

aguccucauc ucccucaagc guuuaagagc uaugcuguuu ugaauggucc caaaac 56

<210> SEQ ID NO 42
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 42

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 43
<211> LENGTH: 100
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 43

aguccucauc ucccucaagc guuuuagagc uaguaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> SEQ ID NO 44
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 44

gcagauguag uguuuccaca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 45
<211> LENGTH: 111
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 45

uccucaucuc ccucaagcgu uuaagagcua ugcugguaac agcauagcaa guuuaaauaa 60

ggcuaguccg uuaucaacuu gaaaaagugg caccgagucg gugcuuuuuu u 111

<210> SEQ ID NO 46
<211> LENGTH: 110
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 46

ccucaucucc cucaagcguu uaagagcuau gcugguaaca gcauagcaag uuuaaauaag 60

gcuaguccgu uaucaacuug aaaaaguggc accgagucgg ugcuuuuuuu 110

<210> SEQ ID NO 47
<211> LENGTH: 114
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 47

gaguccucau cucccucaag cguuuaagag cuaugcuggu aacagcauag caaguuuaaa 60

uaaggcuagu ccguuaucaa cuugaaaaag uggcaccgag ucggugcuuu uuuu 114

<210> SEQ ID NO 48
<211> LENGTH: 115
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 48

ggaguccuca ucucccucaa gcguuuaaga gcuaugcugg uaacagcaua gcaaguuuaa 60

auaaggcuag uccguuauca acuugaaaaa guggcaccga gucggugcuu uuuuu 115

<210> SEQ ID NO 49
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 49

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aauucuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 50
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 50

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaaacuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 51
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 51

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaaacuaguu uguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 52
<211> LENGTH: 111
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 52

ggacuuuuuu uaguccucau cucccucaag cguuuuagag cuagaaauag caaguuaaaa 60

uaaggcuagu ccguuaucaa cuugaaaaag uggcaccgag ucggugcuuu u 111

<210> SEQ ID NO 53
<211> LENGTH: 116
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 53

gaugaggacu uuuuuuaguc cucaucuccc ucaagcguuu uagagcuaga aauagcaagu 60

uaaaauaagg cuaguccguu aucaacuuga aaaaguggca ccgagucggu gcuuuu 116

<210> SEQ ID NO 54
<211> LENGTH: 111
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 54

gcuuguuuuu uaguccucau cucccucaag cguuuuagag cuagaaauag caaguuaaaa 60

uaaggcuagu ccguuaucaa cuugaaaaag uggcaccgag ucggugcuuu u 111

<210> SEQ ID NO 55
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: a is 5'-dimethoxytrityl-adenosine
<222> LOCATION: (1)..(1)

<400> SEQUENCE: 55

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 56
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 56

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 57
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (39)..(39)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other

<400> SEQUENCE: 57

aguccucauc ucccucaagc guuuaagagc uaugcuggna acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 58
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl

<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (39)..(39)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl
<222> LOCATION: (110)..(112)

<400> SEQUENCE: 58

aguccucauc ucccucaagc guuuaagagc uaugcuggna acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 59
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (39)..(39)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (110)..(112)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (110)..(113)

<400> SEQUENCE: 59

aguccucauc ucccucaagc guuuaagagc uaugcuggna acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 60
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (39)..(39)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (39)..(39)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (109)..(111)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (109)..(112)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide

<222> LOCATION: (110)..(112)

<400> SEQUENCE: 60

aguccucauc ucccucaagc guuuaagagc uaugcuggna acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 61
<211> LENGTH: 102
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (2)..(2)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (2)..(2)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (68)..(68)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (68)..(68)
<223> OTHER INFORMATION: n is a, c, g, or u
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (100)..(100)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: n is a, c, g, or u
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (101)..(101)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (101)..(102)

<400> SEQUENCE: 61

ungcagaugu aguguuucca caguuuaaga gcuaguaaua gcaaguuuaa auaaggcuag 60

uccguuanca acuugaaaaa guggcaccga gucggugcun uu 102

<210> SEQ ID NO 62
<211> LENGTH: 100
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (34)..(34)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (34)..(34)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (74)..(74)
<220> FEATURE:

<221> NAME/KEY: misc_feature
<222> LOCATION: (74)..(74)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other
<220> FEATURE:
<221> NAME/KEY: fluorophore
<222> LOCATION: (90)..(90)
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (90)..(90)
<223> OTHER INFORMATION: n is a, c, g, or u, unknown or other
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (99)..(99)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (99)..(100)

<400> SEQUENCE: 62

gcagauguag uguuuccaca guuuaagagc uagnaauagc aaguuuaaau aaggcuaguc 60

cguuaucaac uugnaaaagu ggcaccgagn cggugcuuuu 100

<210> SEQ ID NO 63
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(3)

<400> SEQUENCE: 63

aguccucauc ucccucaagc guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 64
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(4)

<400> SEQUENCE: 64

aguccucauc ucccucaagc guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 65
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(5)

<400> SEQUENCE: 65

aguccucauc ucccucaagc guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 66
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (109)..(113)

<400> SEQUENCE: 66

aguccucauc ucccucaagc guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 67
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (20)..(20)

<400> SEQUENCE: 67

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 68
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (19)..(19)

<400> SEQUENCE: 68

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 69
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (18)..(18)

<400> SEQUENCE: 69

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 70
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (17)..(17)

<400> SEQUENCE: 70

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 71
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (17)..(18)

<400> SEQUENCE: 71

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 72
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (110)..(112)

<400> SEQUENCE: 72

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 73
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (110)..(112)

<400> SEQUENCE: 73

gcagauguag uguuuccaca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 74
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(20)

<400> SEQUENCE: 74

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 75
<211> LENGTH: 113
<212> TYPE: RNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(26)

<400> SEQUENCE: 75

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 76
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(37)

<400> SEQUENCE: 76

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 77
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(7)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (9)..(11)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (13)..(14)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (20)..(20)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (30)..(31)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (33)..(33)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (35)..(36)
<220> FEATURE:
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<222> LOCATION: (42)..(42)
<220> FEATURE:
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<222> LOCATION: (45)..(45)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (76)..(77)
<220> FEATURE:
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<222> LOCATION: (80)..(82)
<220> FEATURE:
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<222> LOCATION: (90)..(90)
<220> FEATURE:
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<222> LOCATION: (95)..(96)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (100)..(101)

<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (104)..(104)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (106)..(112)

<400> SEQUENCE: 77

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 78
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(7)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (9)..(11)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (17)..(17)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (27)..(28)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (30)..(30)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (32)..(33)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (36)..(36)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (39)..(39)
<220> FEATURE:
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<222> LOCATION: (42)..(42)
<220> FEATURE:
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<222> LOCATION: (44)..(44)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (47)..(47)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (57)..(57)
<220> FEATURE:
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<222> LOCATION: (62)..(63)
<220> FEATURE:
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<222> LOCATION: (67)..(68)
<220> FEATURE:
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<222> LOCATION: (73)..(74)
<220> FEATURE:
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<222> LOCATION: (77)..(78)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (87)..(87)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (90)..(90)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (92)..(93)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide

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<222> LOCATION: (97)..(98)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (101)..(101)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (103)..(109)

<400> SEQUENCE: 78

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 79
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(7)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (9)..(11)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (17)..(17)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (27)..(28)
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<400> SEQUENCE: 79

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 80
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
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aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 81
<211> LENGTH: 100
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
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<222> LOCATION: (92)..(93)
<220> FEATURE:
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<222> LOCATION: (95)..(95)

<400> SEQUENCE: 81

aguccucauc ucccucaagc guuuuagagc uaguaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> SEQ ID NO 82
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<220> FEATURE:
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<400> SEQUENCE: 82

gcagauguag uguuuccaca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 83
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<222> LOCATION: (45)..(45)
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<222> LOCATION: (104)..(104)
<220> FEATURE:
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<222> LOCATION: (106)..(112)

<400> SEQUENCE: 83

gcagauguag uguuuccaca guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 84
<211> LENGTH: 100
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
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<220> FEATURE:
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<222> LOCATION: (92)..(93)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (95)..(95)

<400> SEQUENCE: 84

gcagauguag uguuuccaca guuuuagagc uaguaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> SEQ ID NO 85
<211> LENGTH: 100
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<222> LOCATION: (83)..(83)
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<222> LOCATION: (85)..(86)
<220> FEATURE:
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<222> LOCATION: (90)..(91)
<220> FEATURE:
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<222> LOCATION: (94)..(94)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (96)..(99)

<400> SEQUENCE: 85

gcagauguag uguuuccaca guuuuagagc uaguaauagc aaguuaaaau aaggcuaguc 60

cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu 100

<210> SEQ ID NO 86
<211> LENGTH: 113
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-deoxy-nucleotide
<222> LOCATION: (1)..(20)

<400> SEQUENCE: 86

agtcctcatc tccctcaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 87
<211> LENGTH: 113
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-deoxy-nucleotide
<222> LOCATION: (1)..(26)

<400> SEQUENCE: 87

agtcctcatc tccctcaagc gtttaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 88
<211> LENGTH: 113
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-deoxy-nucleotide
<222> LOCATION: (1)..(37)

<400> SEQUENCE: 88

agtcctcatc tccctcaagc gtttaagagc tatgctggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 89
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-deoxy-nucleotide
<222> LOCATION: (15)..(15)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (15)..(16)

<400> SEQUENCE: 89

gcagauguag uguuuccaca guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 90
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)

<400> SEQUENCE: 90

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 91
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(3)

<400> SEQUENCE: 91

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 92
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)

<400> SEQUENCE: 92

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 93
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(5)

<400> SEQUENCE: 93

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 94
<211> LENGTH: 115
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(5)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(6)

<400> SEQUENCE: 94

ggaguccuca ucucccucaa gcguuuaaga gcuaugcugg uaacagcaua gcaaguuuaa 60

auaaggcuag uccguuauca acuugaaaaa guggcaccga gucggugcuu uuuuu 115

<210> SEQ ID NO 95
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (109)..(112)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (109)..(113)

<400> SEQUENCE: 95

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 96
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (108)..(112)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage

<222> LOCATION: (108)..(113)

<400> SEQUENCE: 96

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 97
<211> LENGTH: 114
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 5'-overhang (5' to the 20-nt guide sequence)
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)

<400> SEQUENCE: 97

caguccucau cucccucaag cguuuaagag cuaugcuggu aacagcauag caaguuuaaa 60

uaaggcuagu ccguuaucaa cuugaaaaag uggcaccgag ucggugcuuu uuuu 114

<210> SEQ ID NO 98
<211> LENGTH: 114
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 5'-overhang (5' to the 20-nt guide sequence)
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)

<400> SEQUENCE: 98

gaguccucau cucccucaag cguuuaagag cuaugcuggu aacagcauag caaguuuaaa 60

uaaggcuagu ccguuaucaa cuugaaaaag uggcaccgag ucggugcuuu uuuu 114

<210> SEQ ID NO 99
<211> LENGTH: 115
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 5'-overhang (5' to the 20-nt guide sequence)
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(5)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(6)

<400> SEQUENCE: 99

ucaguccuca ucucccucaa gcguuuaaga gcuaugcugg uaacagcaua gcaaguuuaa 60

auaaggcuag uccguuauca acuugaaaaa guggcaccga gucggugcuu uuuuu 115

<210> SEQ ID NO 100

<211> LENGTH: 115
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 5'-overhang (5' to the 20-nt guide sequence)
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(5)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(6)

<400> SEQUENCE: 100

agaguccuca ucucccucaa gcguuuaaga gcuaugcugg uaacagcaua gcaaguuuaa 60

auaaggcuag uccguuauca acuugaaaaa guggcaccga gucggugcuu uuuuu 115

<210> SEQ ID NO 101
<211> LENGTH: 116
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 5'-overhang (5' to the 20-nt guide sequence)
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(7)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(8)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (112)..(115)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (112)..(116)

<400> SEQUENCE: 101

cucaguccuc aucucccuca agcguuuaag agcuaugcug guaacagcau agcaaguuua 60

aauaaggcua guccguuauc aacuugaaaa aguggcaccg agucggugcu uuuuuu 116

<210> SEQ ID NO 102
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (20)..(20)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (20)..(21)

<400> SEQUENCE: 102

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 103
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide

<222> LOCATION: (19)..(20)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (19)..(20)

<400> SEQUENCE: 103

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 104
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (18)..(18)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (18)..(19)

<400> SEQUENCE: 104

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 105
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (17)..(17)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (17)..(18)

<400> SEQUENCE: 105

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 106
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (17)..(18)
<220> FEATURE:
<221> NAME/KEY: phosphonoacetate internucleotide linkage
<222> LOCATION: (17)..(19)

<400> SEQUENCE: 106

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 107
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:

<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (110)..(112)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (110)..(113)

<400> SEQUENCE: 107

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 108
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (108)..(112)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (108)..(113)

<400> SEQUENCE: 108

gcagauguag uguuuccaca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 109
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(5)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (1)..(6)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (108)..(112)
<220> FEATURE:
<221> NAME/KEY: phosphorothioate internucleotide linkage
<222> LOCATION: (108)..(113)

<400> SEQUENCE: 109

gcagauguag uguuuccaca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 110
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide

<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (110)..(112)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (110)..(113)

<400> SEQUENCE: 110

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 111
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (112)..(112)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (112)..(113)

<400> SEQUENCE: 111

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 112
<211> LENGTH: 75
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (72)..(74)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (72)..(75)

<400> SEQUENCE: 112

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuu 75

<210> SEQ ID NO 113
<211> LENGTH: 77
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)

<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (76)..(76)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (76)..(77)

<400> SEQUENCE: 113

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuauc 77

<210> SEQ ID NO 114
<211> LENGTH: 78
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (77)..(77)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (77)..(78)

<400> SEQUENCE: 114

gaguccucau cucccucaag cguuuaagag cuaugcuggu aacagcauag caaguuuaaa 60

uaaggcuagu ccguuauc 78

<210> SEQ ID NO 115
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(3)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(4)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (110)..(112)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (110)..(113)

<400> SEQUENCE: 115

gcagauguag uguuuccaca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 116
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:

<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (112)..(112)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (112)..(113)

<400> SEQUENCE: 116

gcagauguag uguuuccaca guuuaagagc uaugcuggaa acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 117
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 117

gauguugucg augaaaaagu guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 118
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2-aminoadenosine
<222> LOCATION: (15)..(15)

<400> SEQUENCE: 118

gauguugucg augaaaaagu guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 119
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 119

gauuuagacg aaggauugaa guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 120
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2-aminoadenosine
<222> LOCATION: (15)..(15)

<400> SEQUENCE: 120

gauuuagacg aaggauugaa guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 121

<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (6)..(6)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (8)..(8)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (11)..(11)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (13)..(15)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (31)..(31)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (33)..(33)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (36)..(36)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (39)..(39)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (47)..(47)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (81)..(82)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (90)..(90)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (104)..(104)
<220> FEATURE:
<221> NAME/KEY: 5-methylUridine
<222> LOCATION: (107)..(112)

<400> SEQUENCE: 121

gcagauguag uguuuccaca guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 122
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: Z base
<222> LOCATION: (70)..(71)
<223> OTHER INFORMATION: Z base
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (70)..(71)
<223> OTHER INFORMATION: n is a, c, g, or u, or unknown or other

<400> SEQUENCE: 122

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuagun nguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 123
<211> LENGTH: 100
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl-nucleotide
<222> LOCATION: (54)..(54)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl-nucleotide
<222> LOCATION: (57)..(57)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (99)..(99)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (99)..(100)

<400> SEQUENCE: 123

aguccucauc ucccucaagc guuuaagagc uaguaauagc aaguuuaaau aagguuaauc 60

cguuaucaac aagaaauugu ggcaccgagu cggugcuuuu 100

<210> SEQ ID NO 124
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl-nucleotide
<222> LOCATION: (64)..(64)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl-nucleotide
<222> LOCATION: (67)..(67)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (112)..(112)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (112)..(113)

<400> SEQUENCE: 124

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aagguuaauc cguuaucaac aagaaauugu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 125
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: Z base
<222> LOCATION: (95)..(96)
<223> OTHER INFORMATION: Z base
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (95)..(96)
<223> OTHER INFORMATION: n is a, c, g, or u, or unknown or other

<400> SEQUENCE: 125

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcanngagu cggugcuuuu uuu 113

<210> SEQ ID NO 126
<211> LENGTH: 74
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (73)..(73)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (73)..(74)

<400> SEQUENCE: 126

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguu 74

<210> SEQ ID NO 127
<211> LENGTH: 75
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (1)..(1)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (1)..(2)
<220> FEATURE:
<221> NAME/KEY: 2'-O-Methyl nucleotide
<222> LOCATION: (74)..(74)
<220> FEATURE:
<221> NAME/KEY: thiophosphonoacetate internucleotide linkage
<222> LOCATION: (74)..(75)

<400> SEQUENCE: 127

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguua 75

<210> SEQ ID NO 128
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 128

ttatatgaac ataactcaat ttgtaaaaaa gggtattggg gaattcatta 50

<210> SEQ ID NO 129
<211> LENGTH: 50
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 129

aatatacttg tattgagtta aacatttttt cccataaccc cttaagtaat 50

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<211> LENGTH: 98
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 130

auaacucaau uuguaaaaaa guuuuagagc uauagcaagu uaaaauaagg uaguccguua 60

ucaacuugaa aaaguggcac cgagucggug cuuuuuuu 98

<210> SEQ ID NO 131
<211> LENGTH: 113
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
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<221> NAME/KEY: 2'-deoxy-nucleotide
<222> LOCATION: (1)..(20)

<400> SEQUENCE: 131

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 132
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<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<222> LOCATION: (95)..(96)
<223> OTHER INFORMATION: Z base
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (95)..(96)
<223> OTHER INFORMATION: n is a, c, g, or u, or unknown or other

<400> SEQUENCE: 132

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcanngagu cggugcuuuu uuu 113

<210> SEQ ID NO 133
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
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<221> NAME/KEY: 2'-deoxy-nucleotide
<222> LOCATION: (1)..(37)

<400> SEQUENCE: 133

aguccucauc ucccucaagc guuuaagagc uaugcuggua acagcauagc aaguuuaaau 60

aaggcuaguc cguuaucaac uugaaaaagu ggcaccgagu cggugcuuuu uuu 113

<210> SEQ ID NO 134
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 134

ccagccaagc gcacctaatt tcc 23

<210> SEQ ID NO 135
<211> LENGTH: 88
<212> TYPE: RNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
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<222> LOCATION: (34)..(34)
<223> OTHER INFORMATION: site for fluorescent dye or label attachment

<400> SEQUENCE: 135

ggaaauuagg ugcgcuuggc guuuuagagc uagaaauagc aaguuaaaau aaggcuaguc 60

cgccaucaac uugaaaaagc ggcaccga 88

<210> SEQ ID NO 136
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 136

agtcctcatc tccctcaagc agg 23

<210> SEQ ID NO 137
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 137

cctgcttgag ggagatgagg act 23

<210> SEQ ID NO 138
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 138

agtcctcaac tccctcaagc agg 23

<210> SEQ ID NO 139
<211> LENGTH: 23
<212> TYPE: DNA
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<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 139

cctgcttgag ggagttgagg act 23

<210> SEQ ID NO 140
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 140

agccctcatt tccctcaagc agg 23

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<210> SEQ ID NO 141
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 141

cctgcttgag ggaaatgagg gct 23

<210> SEQ ID NO 142
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 142

actcctcatc cccctcaagc cgg 23

<210> SEQ ID NO 143
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct

<400> SEQUENCE: 143

cctgcttgag ggggatgagg agt 23

We claim:

1. A synthetic CRISPR guide RNA comprising:

(a) a crRNA segment comprising (i) a guide sequence capable of hybridizing to a target sequence in a polynucleotide, (ii) a stem sequence; and

(b) a tracrRNA segment comprising a nucleotide sequence that is partially or completely complementary to the stem sequence,

wherein the synthetic guide RNA has gRNA functionality comprising associating with a Cas protein and targeting the gRNA:Cas protein complex to the target sequence, and comprises one or more modifications in the guide sequence, wherein the one or more modifications comprises a 2'-O-methyl.

2. A method for genome editing to modify a DNA sequence, or for regulating the expression of a gene of interest, or for cleaving a target polynucleotide, or for binding a target polynucleotide comprising: contacting the DNA sequence, the gene of interest, or the target polynucleotide with a CRISPR-associated (Cas) protein and the synthetic guide RNA of claim **1**, and editing, regulating, cleaving, or binding the DNA sequence, the gene of interest, or the target polynucleotide.

3. A set or library of RNA molecules comprising two or more synthetic guide RNAs of claim **1**.

4. The synthetic guide RNA of claim **1** wherein the guide RNA is a single-guide RNA (sgRNA).

5. The synthetic guide RNA of claim **1**, wherein said one or more modifications comprises a 2'-O-methyl nucleotide with a 3'-phosphorothioate.

6. The synthetic guide RNA of claim **1**, wherein said one or more modifications comprises a 2'-O-methyl nucleotide with a 3'-phosphonoacetate.

7. The synthetic guide RNA of claim **1**, wherein said one or more modifications comprises a 2'-O-methyl nucleotide with a 3'-thiophosphonoacetate.

8. The synthetic guide RNA of claim **1** further comprising one or more phosphorothioate internucleotide linkage, phosphonoacetate (PACE) internucleotide linkage, and/or thiophosphonoacetate (thioPACE) internucleotide linkage.

9. The synthetic guide RNA of claim **1**, further comprising up to three phosphorothioate, PACE, and/or thioPACE internucleotide linkages in the guide sequence.

10. The synthetic guide RNA of claim **1**, further comprising up to seven phosphorothioate, PACE, and/or thioPACE internucleotide linkages in the guide sequence.

11. The synthetic guide RNA of claim **1**, further comprising up to ten phosphorothioate, PACE, and/or thioPACE internucleotide linkages in the guide sequence.

12. The synthetic guide RNA of claim **1**, comprising up to five consecutive phosphorothioate internucleotide linkages at a 5'-end of the guide RNA.

13. The synthetic guide RNA of claim **12**, further comprising up to five consecutive phosphorothioate, PACE, and/or thioPACE internucleotide linkages at a 3'-end of the guide RNA.

14. The synthetic guide RNA of claim **1**, further comprising a fluorophore at a 5'-end of the guide RNA.

15. The synthetic guide RNA of claim **1**, comprising one or more end modification.

16. The synthetic guide RNA of claim **1**, comprising at least 2 consecutive 2'-O-methyl modifications.

17. The synthetic guide RNA of claim **1**, comprising at least six 2'-O-methyl modifications.

18. The synthetic guide RNA of claim **1**, comprising at least twenty 2'-O-methyl modifications.

19. A synthetic CRISPR crRNA molecule comprising a guide sequence capable of hybridizing to a target sequence in a polynucleotide, wherein the synthetic crRNA molecule comprises one or more modifications in the guide sequence;

wherein the synthetic crRNA molecule has gRNA functionality comprising associating with a Cas protein and targeting the gRNA:Cas protein complex to the target sequence; and

wherein the one or more modifications comprises a 2'-O-methyl.

20. The synthetic CRISPR crRNA of claim 19, further comprising one or more phosphorothioate internucleotide linkage, phosphonoacetate (PACE) internucleotide linkage, and/or thiophosphonoacetate (thioPACE) internucleotide linkage.

21. The synthetic CRISPR crRNA of claim 19, wherein said one or more modifications comprises a 2'-O-methyl nucleotide with a 3'-phosphorothioate.

22. The synthetic CRISPR crRNA of claim 19, wherein said one or more modifications comprises a 2'-O-methyl nucleotide with a 3'-phosphonoacetate.

23. The synthetic CRISPR crRNA of claim 19, wherein said one or more modifications comprises a 2'-O-methyl nucleotide with a 3'-thiophosphonoacetate.

24. The synthetic CRISPR crRNA of claim 19, further comprising up to three phosphorothioate, PACE, and/or thioPACE internucleotide linkages in the guide sequence.

25. The synthetic CRISPR crRNA of claim 19, further comprising up to seven phosphorothioate, PACE, and/or thioPACE internucleotide linkages in the guide sequence.

26. The synthetic CRISPR crRNA of claim 19, further comprising up to ten phosphorothioate, PACE, and/or thioPACE internucleotide linkages in the guide sequence.

27. The synthetic CRISPR crRNA of claim 19, comprising up to five consecutive phosphorothioate internucleotide linkages at a 5'-end of the crRNA.

28. The synthetic CRISPR crRNA of claim 27, further comprising up to five consecutive phosphorothioate, PACE, and/or thioPACE internucleotide linkages at a 3'-end of the crRNA.

29. The synthetic CRISPR crRNA of claim 19, further comprising a fluorophore at a 5'-end of the crRNA.

30. The synthetic CRISPR crRNA of claim 19, comprising at least 2 consecutive 2'-O-methyl modifications.

31. The synthetic CRISPR crRNA of claim 19, comprising at least six 2'-O-methyl modifications.

32. The synthetic CRISPR crRNA of claim 19, comprising at least twenty 2'-O-methyl modifications.

33. A method for genome editing to modify a DNA sequence, or for regulating the expression of a gene of interest, or for cleaving a target polynucleotide, or for binding a target polynucleotide comprising: contacting the DNA sequence, the gene of interest, or the target polynucleotide with a CRISPR-associated (Cas) protein and the CRISPR crRNA of claim 19, and editing, regulating, cleaving, or binding the DNA sequence, the gene of interest, or the target polynucleotide.

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